Access DB#

28488

## **SEARCH REQUEST FORM**

Scientific and Technical Information Center

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	Requester's Full Name: S. Phone N	() i umber 30 % - 9 34.7	Examiner #: S. De vi	Date: 08 Mayor	)
	Art Unit: // // Phone No. Mail Box and Bldg/Room Location:	CMI- 77-15 Result	s Format Preferred (circle)	PAPER DISK E-MA	IL
	If more than one search is submit	ted, please prioritize	searches in order of n	eed.	***
	Please provide a detailed statement of the se Include the elected species or structures, ke utility of the invention. Define any terms the known. Please attach a copy of the cover sh	ywords, synonyms, acronyr at may have a special mear	ns, and registry numbers, and ning. Give examples or releva	combine with the concept or	
	Title of Invention: Mcuocloi	al antibodie	es against the I	nterperon Roccy	3602
	Inventors (please provide full names):	atrick. Benoit	et al.	F 9000	
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	Earliest Priority Filing Date: 03 *For Sequence Searches Only* Please include	- II - end neut in Commention (no	-	patent numbers) along with the	•
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	Searcher Prep & Review Time:	Fulltext	Sequence Systems	gramma in the deal controllation and any	
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PTO-1590 (1-2000)

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A_Geneseq_36:R57138
A_Geneseq_36:W41804
A_Geneseq_36:R94576
A_Geneseq_36:R7804
A_Geneseq_36:R78911
A_Geneseq_36:R790796
A_Geneseq_36:R10545
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A_Geneseq_36:R75368
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-MODEL-frame+_n2p.model -DEV-xlp
-Q-/Ggn2_1/USPTQ_spool_US09240675/runat_30052000_164311_24603/app_query.fasta.1
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-MAXLEN-100000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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Query length: 401
Database: A_Geneseq_36:*
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A_Geneseq_36
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Database length: 23686106
Search time (sec): 60.370000
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              A_Geneseq_36:R57139
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Mouse II-10 receptor Interleuk
Human gp130 sylice variant. New
Human gp130 N-terminal fragment
gp130 N-terminal fragment. Hete
Human gp130 Fc-His amino acid
Recombinant human gp130 protein
Human soluble glycoprotein (GP)
Human gp130 protein. New splice
Human gp130 rotein. New splice
Human gp130 rotein sibunit
Interleukin-10 receptor subunit
Human interleukin-12 receptor.
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Human interleukin-12
Human interleukin-12
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Gamma-IFN-R-GBP 130 fusion prot
Arabidopsis thaliana ferulate-5
Arabidopsis ferulate-5 hydroxyl
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Human IFN receptor. Compsn. of
Transmembranal interferon alpha
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Complete interferon-alpha/beta
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A_Geneseq_36:W12772
A_Geneseq_36:W93941
A_Geneseq_36:W17859
A_Geneseq_36:W70799
   seq_documentation_block:
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. 24-OCT-1993; IL-107378.
(YEDA) YEDA RES 6 DEV CC
(ABRA/) ABRAMOVICH C.
Abramovich C. P. .
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1. .427
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AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                          lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
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Ratio:
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Gaps:
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ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy

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seq_name: A_Geneseq_36:R14487
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US-09-240-675-1_COPY_27_427
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WP-PSDB; Q14239.

New Mater-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; 52pp; French.

The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.

See also Q14240.
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05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
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Homo sapiens
FR2657881-A.
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Eid P, Gresser I, Lutfalla G, Meyer
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seq_documentation_block:
ID R28495 standard; Prot
AC R28495;
DT 31-MAR-1993 (first e
DE Sequence of a soubble
DE with a high affinity
Interferon receptor;
OS Synthetic.
PN W09218626-A.
PP W09218626-A.
PP 17-APR-1991; W0-F00318.
PR 17-APR-1991; W0-F0031
PR 17-APR-1991; W0
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US-09-240-675-1_COPY_27_427
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Quality:
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SC Claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

Claim 2; Fig 1; 58pp; English.

Claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

Claim 2; Fig 1; Fig 1
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Ratio: 5.203
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17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey M, Uze G;
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R28495;
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Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and beta. Interferon receptor; alpha-interferon; beta-interferon.
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                                                                                                                         AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                   ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                              MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 436
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Gaps: 0
Identity: 100.000
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alignment_scores:
Quality:
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US-09-240-675-1_COPY_27_427 x R71723
                                                                                                                                                                                                                                                                                                                                  Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: A_Geneseq_36:R71723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English.
A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coli or COS cell hosts. The protein was used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens.
WO9507716-A
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IFN receptor extracellular domain.
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interferon-beta; monoclonal antibody; immunomodulator; AIDS
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                                                                                                       CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTXAAATCTCCTC
                                                                                                                                                                           ATGATGGTCGTCCTCCTGGGCGGCGACGACCCTAGTGCTCGTCGCCGTGGG
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   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
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Gaps: 0
Percent Identity: 100.000
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                             alignment_block:
US-09-240-675-1_COPY_27_427 x W21806
                                                                                                                                        alignment_scores:
Align seg
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Align

Ratio: Similarity:

692.00 5.203 100.000

Percent Identity:

Gaps:

133

Quality:

1

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W21806

from: 1

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seq_documentation_block:
ID W21806 standard; Prot
AC W21806,
C W21806;
DT 23-SEP-1997 (first e
DE Spliced-deleted inter
KW Interferon alpha-rece
OS Homo sapiens.
FH Key
FT domain /labe
FT AU9475977-A.
PD 11-MAY-1995.
PF 24-OCT-1994; D75977.
PR 24-OCT-1994; D75977.
PR 24-OCT-1994; D75977.
PR 24-OCT-1994; D75977.
PR 24-OCT-1993; IL-10737.
PR 24-OCT-1994; D75977.
PR 24-OCT-1993; IL-10737.
PR 24-OCT-1994; O75977.
PR 
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New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 3; Fig 7; 46pp; English.

C (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain in transmented by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDAN clore (see also T73521) obtd. From human myeloma U266 cells. Soluble, non-membrane bound IFNAR Splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNA, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed activities of IFNs alpha and beta in cells, tissues and organisms, Sequence 495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1995.
20-0CT-1994; 075977.
24-0CT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LID.
(ABRA/) ABRAMOVICH C.
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Interferon alpha-receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Extracellular_domain
/note= "comprises amino acid residues 1-413
422-427 of transmembranal IFNAR"
420 496
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transmembranal IFNAR"
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seq_name: A_Geneseq_36:R11958
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New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis interferon agonists and in treatment or diagnosis pisclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosist of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are eg where overexpression of alpha-IFN is harmful. The Abs are having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA:
                                                                                                                                                                                                                                                                                                  Human alpha interferon receptor protein.
Human alpha IFN; IFN agonists; antiviral; anti tumour
                                                                                                                                                                                                                                                                                                                                                   R11958 standard;
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                                                                                                                                             WPI; 91-148740/20.
N-PSDB; Q11701.
                                                                                                                                                                   (CNRS ) CNRS CENT NAT RECH SCI.
Mogensen KE, Uze G, Lutfalla G,
                                                                                                                                                                                                                  WO9105862-A.
02-MAY-1991.
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                                                                                                                                                                                                                                                                                                                            19-JUL-1991
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alignment\_scores Ratio: Percent Similarity:

Quality:

692.00 5.203 100.000

Percent

Length: Gaps: Identity:

100.000

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alignment_block:
US-09-240-675-1_COPY_27_427 x R11958
Align seg 1/1 to: R11958
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                                                                                                                                                                                        FR2657881-A.
09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
EId P. Gresser I, Lutfalla G
                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
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                     New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, beta - used to treat e.g. lupus erythematosus, Behcet's disease, beta - used to treat e.g. lupus erythematoid arthritis, etc. aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. pisclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from epitopes are eliminated and the deriv. Block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft
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                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                             Complete interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection;
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                                                                                                                                                                                                                                                                                                                                                                                              R14488 standard;
                                                                                                                                                                 Tovey MG, Uze G; WPI; 91-319778/4
                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                      16-JAN-1992 (first entry)
  rejection.
Sequence
                                                                                                                                                       WPI; 91-319778/44.
N-PSDB; Q14240.
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   See also Q14239.
557 AA;
                                                                                                                                                                                                                                                                                 /label- transmembrane 458. .557
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US-09-240-675-1_COPY_27_427
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Ratio: 5.203
Percent Similarity: 100.000
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water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto: immune diseases and transplant rejection
Claim 3; Fig 2; 58pp; English.
DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (030533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
W09218626-A.
29-OCT-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eid P, Gresser I, Lutfalla G, Me
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Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
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31-MAR-1993
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US-09-240-675-1_COPY_27_427 x R28496
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R42635 standard; Property
          EP-563487-A.
06-CCT-1993;
31-MAR-1992; 400902.
31-MAR-1992; EP-400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE S.
Benoit P, Maguire D, Meyer F, I
WPI; 93-312951/40.
P-PSDB; R42635.
                                                                                                                                                                                        Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
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                                                                                                                                                      domain
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100.000
                                                                                                                  1. .436
/label- extracellular_domain
/name_ "soluble, immunogenic
                                                                                                                                                                  Location/Qualifiers
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 human
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                                                                                                                            of IFN-R
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alignment_block:
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Ratio: 5.203
Percent Similarity: 100.000
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                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibodies produced against soluble forms of the hu interferon alpha-beta receptor based on the full-length human sequence are claimed. The antibodies are useful for treatment prophylaxis of disorders involving cell proliferation and/or v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neutralising activity against human type I interferon, therapy and diagnosis Disclosure; Fig 3; 21pp; English.
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 16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizari EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                   Human IFN receptor
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                                                                                                                  Homo sapiens.
                                                                                                                            IFN receptor; int
interferon-beta;
                                                                                                                                                              16-OCT-1995 (first entry)
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                                                         23-MAR-1995
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ta; monoclonal antibody; immunomodulato
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alignment_scores:
Quality:
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 PRETTT TENE
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                                                                                                                                                                                        documentation_block:
W21804 standard; Pr
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Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.

The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.

Sequence 557 AA;
AU9475977-A.
11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
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Ratio: 5.203
Similarity: 100.000
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                                 __el= Extracellular_domain
437. .457
/label= Transmembrane /
458. .557
/label= In+
 075977.
IL-107378.
                                                                                                                                          interferon alpha-receptor.
ha-receptor; IFNAR.
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Ratio: 5.203
Percent Similarity: 100.000
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New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) plsclosure; Fig 7: 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polyapetides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                  20-NOV 1998 (first entry)

20-NOV 1998 (first entry)

20-NOV 1998 (first entry)

20-YOT7 cytokine receptor; polypeptide, polypeptide; kidney; pancreas;

20-YOT7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;

type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;

agonist; cell proliferation; cell differentiation; renal disease; human;

neural disease; pancreatic disease.
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(ABRA/) ABRAMOVICH C.
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Location/Qualifiers
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Percent Identity: 100.000
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CC This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-composition of the zcytor containing the Zcytor CC This represents the Zcytor7 cytokine receptor containing the Zcytor CC receptor family (CRF2). An expression vector containing the Zcytor CC receptor family (cRF2). An expression vector containing the Zcytor CC concoding a transmembrane and intracellular domain, or both, and a CC transcriptional terminator can be used to transform host cells for the CC transcriptional terminator can be used to transcriptional terminator of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is C tissue. Agonists of Zcytor7 can be used to stimulate proliferation and CC differentiation of cell in these organs. The antagonists and agonists can calso be used in the treatment of renal, neural, pancreatic and prostate
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27-AUG-1998.
18-FEB-1998; UO3029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
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Adams RL, Farrah TM, Jelm
Whitmore TE;
WPI; 98-480798/41.
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N-PSDB; V57515.
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                                                                                                                                                                                           uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA
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                                    TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh
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                                                                 GAAAAAGAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                    CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA...
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Ratio:
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/note= "extracellular (ligand-binding) domain:
/sequence claimed in claim 1"
275. .553
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62.205
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seq_documentation_block:
ID W52296 standard; Prot
AC W52296;
DT 23-JUN-1998 (first (
DT 23-JUN-1996 (JIN-1997 
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PS Claim 2; Page -; 79pp; English.

CC rimis sequence is the human CRFB4 sequence, DNA encoding it is used in the CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1) CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2) CC encoding CRFB4, both operably linked to expression control sequences. CC cells containing (I) may be used to identify agonists/antagonist of CC cells containing (I) may be used to identify agonists/antagonists are potentially useful, e.g. for preventing allograft CC rejection, as vaccine adjuvants, for treatment of photosensitivity. CC rejection, as vaccine adjuvants, for treatment of photosensitivity contributed in the contributed contributed in the contributed in the contributed contr
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US-09-240-675-1_COPY_27_427 x w52296
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Ratio:
Percent Similarity:
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17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
Kotenko SV, Pestka S;
WPI; 98-110590/10.
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                                              184
                                                                                                                                                                                                                       134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
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                                                                                                                                  snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
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Human cytokine receptor 11 (Zcytor11).
Cytokine receptor 11; Zcytor11; human; pancreas; small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                   Novel human cytokine receptor Zcytorll - use ligands to modulate or promote proliferation of e.g. pancreatic or colon tissue Claim 27; Page 54-56; 62pp; English.
                                                                                                                                                                                      (ZYMO) ZYMOGENETICS INC. Adams RL, Farrah TM, Jelmberg WPI; 99-167425/14.
                                                                                                                                                                                                                                                          18-FEB-1999.
30-JUL-1998; U15847.
05-AUG-1997; US-906713
This is the amino acid sequence of human cytokine receptor 11 (2cytor11), a novel class II cytokine receptor that appears to be receptor for a helical cytokine of the interferon/interleukin-10
                                                                                                                                                                   N-PSDB; X24379
                                                                                                                                                                                                                                                                                                                             WO9907848-A1.
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alignment_block:
US-09-240-675-1_COPY_27_427 x w97861
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Percent Similarity:
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                                                                                                                                                                                                         documentation_block:
R75782 standard; Protein; 332
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/label- Extracelular_domain
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alignment_block:
US-09-240-675-1_COPY_27_427 x R75782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOEH/) BOEHNI R.
(HEMM/) HEMMI S.
Aguet M. Boehni R,
WPI; 95-224321/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig.2A; 86pp; English.

The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be may be used to treat pathological conditions associated with endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGUE/) AGUET M.
(BOEH/) BOEHNI P
                                                                                            310 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC
                                                                                                                                                                                                                               228
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07-DEC-1994;
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                              357 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396
                                                                                                                                                                                                                                                                                            181 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT
                                                                                                                                                                                                                                                                                                                                                               149
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                                                                                                                                                            IFN-gamma production.
Sequence 332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TTGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC
                                                             valArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr
                                                                                                                                                                                                                                                                                                                                                                                              oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
oPheGlnHisTyrGluAsnValThrValGlyProProLys
                                                                                                                                                                                               uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG
                                                                                                                                                                                                                             G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                             luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
                                                                                                                                                                                                                                                                                                                                                            ACAGGAGCGATGAGTCT......GTCGGGAATGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 148
                                                                                                                               lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
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/label= Cytoplasmic_domain
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/label- Transmembrane_anchoring_domain
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Page 10

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Sequence
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Database length: 14437401
Search time (sec): 65.1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query length: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search information block:
Query: US-09-240-675-1_COPY_27_427
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-Q-/cgn2_1/USPT0_spco1/US09240675/runat_30052000_164312_24612/app_query.fasta.1
-DB-ISsued_Patents_AA -QFMT-fastan -SUFFIX-modif.rai
-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-COOPEXT-0.000 -QGAPOP-4.500 -OGAPEXT-0.050 -XGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -FGAPOEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-DLOSUM62 -TRANS-human40.Cdi -LIST-45 -DCALIGN-200
-THR_SCORE-pct -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -MORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3
-NO_XLPXY -WARI -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Results were produced by Copyright (c) 1993-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-1_COPY_27_427
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Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           software, version
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8.2e-1
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             .8e-07 574
2 1.7e-07
5 9.0e-07
2 1.8e-05
3 0.0025
4 0.0063
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                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-328-256-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
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APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
APPLICANT: RATOVITSKI, Edward
APPLICANT: NVENTION: SOLUBLE INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICAN: SOLUBLE INTELLE OF INVENTION: SOLUBLE INTELLE OF INVENTION: PREPARATION PREPARATION OF SECUENCES: 12
         101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
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                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROWDY, Roger L. REGISTRATION NUMBER: F
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-328-256-11
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/Cgn2_6/ptodata/1/iaa/5a_COMB.pep:US-09-091-432-2 + 
/Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-424-788-5 + 
/Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-110-683-2 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

APMER BROWNE BOGGET!
                ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGG
                                                                                                                                                             Gaps:
Percent Identity:
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578
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lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn

50

AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200

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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-2
; MOLECULE TYPE: US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2,
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION UMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                            TELEPHONE: (202)672-539 TELEFAX: (202)672-539 ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                   SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 177
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C. 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BENOIT, Patrick
BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
TOVEY, Michael G.
NVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
NVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
                                                                         436 amino acids
                                                                                                                              (202)672-5399
                                                                                                                                                   (202)672-5300
                   protein
                                                                                                                                                                                                                                                                                                                                    PCT/EP93/00770
                                                                                                              2:
                                                                                                                                                                                      17283/117/GUPL
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alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-307-588-2
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Patent No. !
SOFTWARE: PATENTIN Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: IL 107378
FILING DATE: 24-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE BROWDY AND NEIMARK
THORSES:
THE STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
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                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
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5643749
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alignment_block:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12
                                                                                                                                                                                                                                            seq_documentation_block:
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                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10
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Ratio: 5.203
Percent Similarity: 100.000
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
                                                                                                                                                                                                Sequence 10, Application US/08328256 Patent No. 5643749
                           GENERAL INFORMATION: APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                            101
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
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                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                         LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 100.000
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alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-328-256-10
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-/--
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
FUNGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-328-256-10 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                   151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                   101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                         251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                       201 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATAFTACTA 250
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TYPE: amino acid
STRANDEDNESS: single
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                                        AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                            erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                             sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                              lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
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ER: 25,618
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Percent Identity: 100.000
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TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399

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seq_documentation_block:
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                                                                                                                                                                                                                                                alignment_block:
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                                                                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                               Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/900,642
APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERAPING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GRESSER, ION
TITLE OF INVENTION: THE ALPHA INVERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: THE ALPHA INVERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                              CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
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5731169
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linear
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5.203
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seq_documentation_block:
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                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                  TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOGENSEN, KNU
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Gec
APPLICANT: GRESSER, ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
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                                                                                                                                                                                                 APPLICATION: 20-OC1-1.
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMAS E.
THOMAS E.
32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                              REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 20,205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
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                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                   TELEPHONE: (/v-/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
      LENGTH: 50.
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                    amino acids
acid
single
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linear

protein

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alignment_scores;
Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
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; MOLECULE TYPE:
US-08-466-974-2
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US-09-240-675-1_COPY_27_427 x US-08-466-974-2
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08471453 Patent No. 5886153
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR THE TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
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                                                                                                         COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                   STREET:
                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                 1100 NORTH GLEBE ROAD
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; MOLECULE TYPE:
US-08-471-453-2
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US-09-240-675-1_COPY_27_427 x US-08-471-453-2
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Ratio: 5.203
Percent Similarity: 100.000
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 anino acids
TYPE: anino acid
STRANDEDNESS: single
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APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7
 117
                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                              301
                                                                                                                                                                                                                                            201 AACTGGGATGGATAATTGGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                           151
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                                                                                                                                                                                                                                                                                                                                                                                                                  101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                          34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                   TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                      AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                       GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                         AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
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linear
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Percent Identity: 100.000
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seq\_documentation\_block:
; Sequence 4, Application US/08307588

seq\_name: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:US-08-307-588-4

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alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-4
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)672-3399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/EP
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 924
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: D.C.
STATE: D.C.
20007
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APPLICANT: TOVEY, MICHAEL G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 17283/117/GUPL
                                                                                                                                                                                                                                             yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                    CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                        ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGUIRE, Deborah
PLAVEC, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BENOIT, Patrick
MEYER, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            692.00
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alignment_block:
US-09-240-675-1_COPY_27_427 x PCT-US94-14277-3
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                                                                                                                                                                                    alignment_scores:
Quality:
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                                                                                                                                                                                                                                                            ; TOPOLOGY: PCT-US94-14277-3
                                                                                                                                               Ratio:
Percent Similarity:
                                                    Align seg 1/1 to: PCT-US94-14277-3 from: 1 to: 202
                                                                                                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: LOVE, RICHARD B.
REGISTATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOSTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/164596 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
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T: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                 202 amino acids
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                                                                                                                                               273.50
3.552
71.963
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                                                                                                                                                 Percent Identity: 48.598
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                                                                                                                                                                                    Length:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 HisMetSerProProGluVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 ..ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803/305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 GAATGTTTATGAAGAAATTAAAT%GCGTATAAGAGCAGAAAAAGAAAAAC. 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 181
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                             REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 erThrSerSerTrpAsnGluValAspProPheIleProPheTyrThrAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 rAsn***TyrIleLysThrGlnPheArgValArgAlaGluGluGlyAsnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 GluCysGlnHisThrThrThrThrLysCysGluPheSerLeuLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 heSerAlaGluTyrArgThrLysAspGluArgLysTrpLeuLys***Pro 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
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                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1201 E
                                                                                                                                                     TELEFAX:
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                TYPE: amino acid
STRANDEDNESS: sir
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STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGATTGGTCCTCCAGAAGTA 399
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T: Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WA
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                                                                                                                                                     206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                  single
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US-09-240-675-1_COPY_27_427 x US-08-943-087-2
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; FRAGMENT TYPE:
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                       APPLICANT: LOK, Si
APPLICANT: Kho, Choon J
APPLICANT: Jelmberg, Ann
APPLICANT: Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 eLeuGluThrGlnIleGlyProProGluVal 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG...
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Farrah, Theresa M. TITLE OF INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 AGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                   CITY: Seattle
STATE: WA
                                                                                                          COUNTRY: UZIP: 98102
                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, Application US/08943087 5945511
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                                                                                                                                                                                               E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                   Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                Whitmore,
FastSEQ for Windows Version
                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146.00
1.848
62.205
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                                                                                                                                                                                                                                                                                                                                Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 29.921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
  2.0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087

CLASSIFICATION: 536

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alignment_scores:
Quality:
Ratio:
seq_documentation_block:
; Sequence 16, Application US/08943087
; Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
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                                                                                             seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-240-675-1_COPY_27_427 x US-08-943-087-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                             132 eLeuGluThrGlnIleGlyProProGluVal 142
                                                                                                                                                                                                                                                                                                                                                                                   272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                                                                          116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                          319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                     82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
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                                                                                                                                                                                                                                                                                                                                          laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                             TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
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linear
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; TOPOLOGY: 1in
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-943-087-16 from: 1 to: 553
                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
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                                                                                                125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
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TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                    66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                           49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                     34 rGlyGly.....LeuProLySProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                              75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                   18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                       31 CTAGTGCTCGTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 98102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/943,087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 553 amino acids amino acid
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Adams, Robyn L.
Whitmore, Theodore E.
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internal
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
                                                                                                                                                    FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                    nt Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/943,087 FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                          STRANDEDNESS:
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                                      Ratio:
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Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
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internal
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                                      146.00
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                                                                                                                                                                                                                                                                                         18:
                  Percent Identity: 29.921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence
                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lok, S1
APPLICANT: Kho, Choon J
APPLICANT: Jelmberg, Anı
                                ATTORNEY/AGENT INFORMATION:
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Farrah, Theresa M.
                                                                                                                                                                                                      COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                              FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eLeuGluThrGlnIleGlyProProGluVal 142
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                                                                                                                                                                                                                                                                                                                                             Seattle
                                                                                                                                                                                                                                                                                                                             WA
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                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                             1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jelmberg, Anna
Adams, Robyn L
                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                   ZymoGenetics,
Paul G
NUMBER:
                                                                        08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anna C.
                                                                                                                                                    US/08/943,087
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East

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alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-18
                                                                    272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                             222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                                                                                                                                                                                                                                                                                    125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                                                                                                                                                                                                                                                                            49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                            66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
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                                                                                                                                            uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
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REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELLEPHONE: 206-442-6627
TELLEPHA: 206-442-6678

96-24C1

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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-20
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US-09-240-675-1_COPY_27_427 x US-08-943-087-20
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                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-22
                                                                                                                                                                                                                                                                              seq_documentation_block:
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                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                   Sequence 22, Application US/08943087 Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
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APPLICANT: Whitmore, Theodore E. APPLICANT: FAIRAh, Theresa M. TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                              APPLICANT: Lok, S1
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
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                                                                                                                                                                                                                                                                                                                                                                             eLeuGluThrGlnIleGlyProProGluVal 142
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TOPOLOGY: 11n;
MOLECULE TYPE:
FRAGMENT TYPE:
US-08-943-087-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
319 GAAAAAGAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
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                                                                                                                                                                                  222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                   272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                         99 laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                            82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                              66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe
                                                                                                                                                                                                                                                                                                             49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                 34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                        75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1201 :
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/943,087 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Gaps:
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pir2:S61405
pir2:A41734
pir2:T34345
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Ouery: US-09-240-675-1_COPY_27_427
Ouery length: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000
                                                                                                                                                                                                                        pir2:S36638
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pir2:T22836
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pir2:A49667
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pir2:JC6311
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pir2:S27387
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-0-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-0-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-DB-PIR_63 -QFMT-fastan -SUFFIX-modif.rpr -GAPOP=12.000
-GAPEXT-4.000 -MIMATCH-0.100 -LOOPEXT-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -BELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALION-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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2:S67208
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+ 365.50
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Documentation
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pir2:A48584
pir2:A45731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_27_427 x A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-557 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: A32694 from: 1 to: 557
                                                   251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                     201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                         AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                             erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                    sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
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Percent Identity:

Length:

133

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50 150 100 17

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A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Gross-references: GDB:120078; OMIM:107450
A;Gross-references: GDB:120078; OMIM:107450
A;Gross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-21/Domain: transmembrane #status predicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha/Seta receptor precursor - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 22-Jun-1990 *sequence_revision 22-Jun-1990 *text_change 22-Oct-1999 (C;Accession: A32694; S17112 (R;Uze, G.; Lutfalla, G.; Gresser, I. (cell 60, 225-234, 1990 (R;Title: Genetic transfer of a functional human interferon alpha receptor into mou. A;Title: Genetic transfer of a functional human interferon alpha receptor into mou. A;Reference number: A32694; MUID:90124632 A;Accession: A32694
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A; Cross-references: EMBL: X60459; NID: g32671
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: The structuree of the human interferon alpha/beta receptor gene. A;Reference number: $17112 A;Accession: $17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
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! transmission blocking ta:
! comC-alpha protein - phag:
! neutrophil gelatinase-ass:
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421,'Y',423-560 <LIM>
A;Cross-references: EMBL:LO6320; NID:g163187; PIDN:AAA02571.1; PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1173, 314-319, 1993 A;Title: Cloning and characterization of a A;Reference number: S33770; MUID:93305725 A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Specific antiviral activities of A; Reference number: S27387; MUID:93076908 A; Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: antiviral; cytokine receptor; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG> F;25-560/Product: interferon alpha receptor type 1 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-560 <MOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                                                                         254 CCAAATGCAACTTTTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT 300
                                                                                                                                                                                 154 AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.K.; Langer, J.A
                                                                                                                                                                                                                                                                                                                                                           54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                         16 gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                     TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                            uGlyThrAspAsnTrpLysLysLeuSerGlyCysGlnHisIleThrSerT
                                                                                                                  TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                                                                                            SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGlnIleLe
hrLysCysAsnPheSerSerValGluLeuGluAsnValPheGluLysIle
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Ratio:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-590 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 265-375 < RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 127-224 <RE2>
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A; Residues: 118-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 148, 343-346, 1994
                       A; Gene: IFNAR
A; Introns: 177/3; 331/1
                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: I48426
                                                                                                                                                                                                                                                                  A; Accession: I48428
      ;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 al 132
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                                                                                                       <RE7>
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interferon alpha/Deta receptor - mouse C:Species: Mus musculus (house mouse) C:Species: Mus musculus (house mouse) C:Date: 25-Mar-1993 *sequence_revision 18-Nov-1994 *text_change 05-Nov-1999 C:Date: 25-Mar-1993 *sequence_revision 18-Nov-1994 *text_change 05-Nov-1999 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429 R:Uze, G:; Lutfalla, G:; Bandu, M.T.; Proudhon, D:; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A;Reference number: A45283; MUID:92262522
                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ.
A;Molecule type: DNA
A;Residues: 426-445 <RE6>
A;Cross references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1;
A;Accession: 148429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: A;Reference number: I48423; MUID:95047447
A;Accession: I48423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted from NCBI backbone R; Lutfalla, G.; Uze, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1;
A;Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
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A;Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 GluLeuArgIleArgAlaGluGluGlyAsnAsnThrSerThrTrpTyrGl 115
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NCBIP: 102357)
              PID:g510265
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protein

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alignment_block:
US-09-240-675-1_COPY_27_427 x A45283
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A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: G06935
A; Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytokine receptor family II, member 4 - human
C; Species: Homo sapiens (man)
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'ignment_block:
'-09-240-675-1_COPY_27_427 x G01418
                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheArgValArgAlaGluGluGlyAsnSerThrSerSerTrpAsnGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCGTATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrLysCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sAspGluAlaLysTrpLeuLysValProGluCysGlnHisThrThrThrT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oTrpValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA 34
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78.195
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1.896
59.504
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Percent Identity:
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                                                                              33.058
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alignment_block:
US-09-240-675-1_COPY_27_427 x A47003
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C; Keywords: transmer
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A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A new member of the cytokine receptor gene family maps on A;Reference number: A47003; MUID:93300510
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A;Title: A new member of t
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C;Species: Homo st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Lutfalla, G.; Gardiner, K.; Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A47003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
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                                         97 ......CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                      ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC
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yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                    TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                               TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane proțein
                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                             Ratio:
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1.896
59.504
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                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                             to: 325
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                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                      33.058
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21 a:

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seq_name: pir2:JC6311
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A; Accession: JC6311
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R;Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_427 x JC6311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U53696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: JC6311 from: 1 to: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 GATTGGTCCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
146 GGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAT 195
                                                                                                 57 GluSerTyrArgSerPheGlnAspHis...
                                                                                                                                                                                            40 rpGluValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                         23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGlnT 40
                                                                                                                                                                                                                                                                                                                                         96 TCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATC
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|HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eIleGlyProPro 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA....AAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 239
                                                                                                                                                                                                                                                                                                                                                                                        LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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1.693
61.983
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                                                                                                 .....CysLy
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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEMY
A:Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A:Cross-references: early B-cell line Y16
A:Experimental source: early B-cell backbone (NCBIN:145654, NCBIP:145656)
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C:Keywords: cytokine receptor
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R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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US-09-240-675-1_COPY_27_427 x A49947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 TCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 ATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAACACTTCT 336
                                                                                                                                                                                                                                                                                                                   228
                                                                                                                                                                                                                                                                                                                                                                                                              181 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 ACAGGAGCGATGAGTCT......GTCGGGAATGTGACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 GluTrpValAsnVal...ThrPheCysProValGluAspThrIleIleGl 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 yrGlyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG 49
                                                                                                                                                       93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LeuGlyAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TTGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC 98
                                                                                             ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 356
ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396
                                              ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                           G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                  luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu 65
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1.500
61.538
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Percent Identity:
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30.769
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interferon-gamma receptor

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C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, Scell 76, 793-802, 1994
A;Title: Identification and sequence of an accessory factor required for activation of A;Reference number: A49946; MUID:94170380
A;Accession: I38500
A;Accession: I38500
A;Residues: 1-337 <RESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-63,'Q',65-337 <RE2>
A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
A;Experimental source: clone pJS3
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C; Keywords: cytoki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords: cytokine receptor
                                                                                                                                                                            104 GlyPheProMetAspPheAsnVal......ThrLeuArgLeuAr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 AGAATATTACTAGTACCAAATGCAACTTTTCTTCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 ATGACAACTTTATCCTGAGGTGG.......AACAGGAGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 ArgProValValTyrArgValGlnPheLysTyrThrAspSerLys.... 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaProProAs
   CACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA
                                                          gAlaGluLeuGlyAlaLeuHisSerAlaTrpValThrMetProTrpPheG
                                                                                                                     AGCAGAAAAAGAAAACACT...TCTTCATGGTATGAGGTTGACTCATTTA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt snAlaGluGlnValLeuSerTrpGluProValAlaLeuSerAsnSerThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA 42
                                                                                                                                                                                                                                                                                              hrGlnIleThrAlaThrGluCysAspPheThrAlaAlaSerProSerAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG
                                                                                                                                                                                                                                    .....CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAG 314
                                                                                                                                                                                                                                                                                                                                                                                                                .......TrpPheThrAlaAspIleMetSerIleGlyValAsnCysT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
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1.393
51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein
seq_name: pir2:T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-240-675-1_COPY_27_427 x A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A31555
R;Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of the A;Reference number: A31555, MUID:89003065
A;Accession: A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-489 <AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interferon gamma receptor precursor - human
C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: A31555 from: 1 to: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                          130
                                                                                                                  392 CAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133
                                                                                                                                                                         113 rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                                                                                                                                                    342 GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATG
                                                                                                                                                                                                                                                                                           TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy 113
                                                                                                                                                                                                                                                                                                                                                      AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                             isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
                                                    roLysLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lnHisTyrArgAsnValThrValGlyProProGlu 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.50
1.018
61.765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-Feb-1990 #text_change 23-Jul-1999
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42

130 391 98

65

Genetics:

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submitted to the EMBL Data Library, May 1996 A;Reference number: Z20442 A;Accession: T27934
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T27934; T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
144/3; 6683/3; 6768/1; 6800/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-6831 <WIZ>
A; Cross-references: EMBL: Z73899;
A; Experimental source: clone ZK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-6831 <WIL>
A;Cross-references: EMBL:273897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.la
A;Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_427 x T27934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
seq_name: pir2:S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: T27934 from: 1 to: 6831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                        1919
                                                         1967 1 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1906 TrpValPro......CysAlaLysValLysAspThrLysAlaH1sIl 1919
                                                                                                                                                                  1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1889 luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg 1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1856 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 ATGTGACTTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 CTAAAATCTCCTCAAAAA.......GTAGAGGTC...GACATCAT 122
                                                                                                                                                                                                                laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr
                                                                                                                                                                                                                                                                                                                              CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                        eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG 1889
                                                                                                                 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 117
Gaps: 8
Percent Identity: 26.496
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                                                                                                                                                                        1967
                                                                                                                                                                                                                                                                                1950
                                                                                                                                                                                                                            398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
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N;Alternate names: myosin-regulating protein
N;Contains: protein Kinase (EC 2.7.1.-)
C;Species: Caenorhabditis elegans
C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 18-Jun-1999
C;Accession: S57242; S07571; S06797; S57218
R;Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
submitted to the EMBL Data Library, February 1993
A;Description: Additional sequence complexity within twitching of Caenorhabditis ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Map position: IV
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 582/.
152/3; 6691/3; 6776/1; 6808/3
C:Superfamily: twitchin: fibronectin type III repeat homology: immunoglobulin homology: experimently: twitchin: fibronectin: duplication: muscle: phosphotransferase: serin: c:Keywords: ATP: autophosphorylation: duplication: muscle: phosphotransferase: serin: c:Keywords: ATP: autophosphorylation: duplication: muscle: phosphotransferase: serin: c:Keywords: ATP: autophosphorylation: duplication: muscle: phosphotransferase: serin: c:Keywords: ATP: 1083.018-1175.118-1273.1474-1567.170-1864,2066-2158,2358-2.
96-5790.6263-6356,6386-6478.6541-6635.6649-6742,6745-6838/Region: motif 2
F;1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2-23,4215-4313,4314-4415,4416-4516,4612-4710,4711-4811,4908-5009,5010-5109,5110-5210, F;5940-6197/Domain: protein kinase homology <KIND
F;5940-6197/Domain: protein kinase homology <KIND
F;5948-9956/Region: protein kinase ATP-binding motif
F;5971/Active site: Lys *status predicted
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A:Experimental source: var. Bristol
R:Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A:Title: Sequence of an unusually large protein implicated in regulation of myosin & A:Accession: S06797; MUID:90044042
A:Accession: S06797
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A; Accession: S07571
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                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_427 x S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
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A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Experimental source: var. Bristol
C;Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,
A; Cross_references: EMBB:X11423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 792-6839 <BEN2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: var. Bristol
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A;Residues: 1-6839 <BEN1>
A;Cross-references: EMBL:L10351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown
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                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
88 CTANAATCTCCTCAAAAA......GTAGAGGTC...GACATCAT 122
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                                                                                                                                         to: S57242 from: 1 to: 6839
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1.151
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8
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1864 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh

2263

2279

2296

266

2248

2218

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seq_documentation_block:
hypothetical protein ZK617.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T27935; T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x T27935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, May 1996 A; Reference number: Z20458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-7160 <WIL>
A; Cross-references: EMBL: 273897;
A; Experimental source: clone ZK61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: p1r2:T27935
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A; Accession: T27935
                                                                                                                                                                                                                                                                                                                                                           h;Map position: 4
h;Introns: 10/3; 61/3; 
3067/1; 3141/3; 3269/1;
                                                                              Align seg 1/1
                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: CESP: ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reference number: Accession: T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status:
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                       88 CTAAAATCTCCTCAAAAA...
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                                                                              to: T27935
                                                                                                                                                                                                     84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                           135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 6473/3; 7012/3; 7097/1; 7129/3
                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    997; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
ZK617
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                                                                              to: 7160
.GTAGAGGTC..
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                                                                                                                                                                                                                                                                                                                                                                                   542/3; 574/3;
                     A;Cross-references: EMBL:X95644; NID:gll99535; PIDN:CAA64904.1; PID:e223186; PID:g
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain $288C
R;BosKovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.;
submitted to the EMBL Data Library, February 1996
A;Reference number: $67406
A;Accession: $67410
                                                                                                                                                                                     Yeast 12, 1077-1084, 1996
A;Title: The sequence of a 20.3 kb DNA fragment from the left arm A;Reference number: $72094; MUID:97051597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the Protein Sequence A; Reference number: S67629 A; Accession: S67650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X04423; NID:g3848; PIDN:CAA28019.1; PID:g3849 R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-306 <BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Saccharomyces cerevisiae
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988
C;Accession: A25698; S67650; S67410; S72098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable protein kinase KIN28 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N; Alternate names: protein D2330; protein YDL108w
                                                                                              A; Molecule type: DNA
A; Residues: 1-306 <SAI>
                                                                                                                                                   A;Status: nucleic acid sequence
                                                                                                                                                                             A; Accession:
                                                                                                                                                                                                                                                                                    R;Saiz,
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-306 <BOS>
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A; Residues: 1-306 <SIM>
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                                                                                                                                                                                                                                                  Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64904.1; PID:e223186; Saiz, J.E.; Bultrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F. mast 12, 1077-1084, 1996
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                                                                                                                                                      not shown; translation not shown
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18-Jun-1999

Ö.

Saccharomyces

PID:9

Revuelta, J.L.;

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C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase F;5-259/Domain: protein kinase homology <KIN>F;13-21/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_27_427 x A25698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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A; Introns: 10/1
        C;Superfamily: human cyto C;Keywords: heme; iron; o F;458/Binding site: heme
                                                                                                                                                                                                                                                                                                 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; E submitted to the Protein Sequence Database, March A:Reference number: Z15378
A:Accession: T04591
                                                                                                                                                                                                                                                                                                                                                                                                  ferulate-5-hydroxylase (EC 1....) - Arabidopsis thaliana
N;Alternate names: cytochrome P450-dependent monooxygenase; protein F23E13.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 29-Sep-1999
C;Accession: T04591
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-520 <BEV>
A; Cross-references: EMBL: AL022141
                                        A;Introns: 171/1; 314/3
A;Note: F23E13.110
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: heme; iron; oxidoreductase
                                                                                                                                                                      A; Experimental source: cultivar Columbia; BAC C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:T04591
                                                                                                                                                A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: A25698 from: 1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 CCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 spTrpProGluValSerSerPheMetThrTyrAsnLysLeuGlnIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 CATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 PheAlaGluLeuMetLeuArgIleProTyrLeuProGlyGlnAsnAspVa 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 leTrp.....SerValGlyValIle 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAAC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTCTTCACTCAAGCTG...........AATGTTTA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluIleLeuThrSerAsnValValThrArgTrpTyrArgAlaProGlu..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lAspGlnMetGluValThrPheArgAlaLeuGlyThrProThrAspArgA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....LeuLeuPheGlyAlaLysHisTyrThrSerAlaIleAspI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProPro 246
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1.606
50.980
                     iron
                (Cys) (axial ligand) #status predicted
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Gaps: 4
Percent Identity: 26.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306
                                                                                                                                                                                                                                                                                                                                                       E.; Brandt, A.; Duesterhoeft, A.;
March 1998
                                                                                                                                                                                                   clone F23E13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
                                                                                                                                                                                                                                                                                                                                                                                    Jesse,
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alignment_scores:
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Ratio:
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alignment\_scores:

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A; Experimental source: cultivar Columbia; C; Genetics:
A; Map position: 4
A; Introns: 47/3; 130/3; 163/1; 262/2
A; Note: F14M19.130
                                                                                                                                                                                                                                                                                           R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Hoheisel, submitted to the Protein Sequence Database, March 1999
A;Reference number: 215262
A;Accession: T04239
A;Rolecule type: DNA
A;Residues: 1-378 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein r14M19.130 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C;Accession: T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL049480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: T04591 from: 1 to: 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 CAGATTGGTCCTCCAGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCT........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 luAspLeuLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .GluTrpAlaLeuThr................GluLeuLeuArgSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluProGlyValProAsp 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spProThrSerTrpThrAspProAspThrPheArgProSerArgPheLeu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eIleProLysLysSerArgValMetIleAsnAlaPheAlaIleGlyArgA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLeuLeuHisGluThrAlaGluAspThrSerIleAspGlyPhePh 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yrLeuLysCysThrLeuLysGlu...ThrLeuArgMetHisProProIle 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .valGlyLeuAspArgValGluGluSerAspIleGluLysLeuThrT 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT
Quality:
Ratio:
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1.137
46.795
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  Length:
Gaps:
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6
21.154
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alignment_block:
US-09-240-675-1_COPY_27_427 x T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T04239 from: 1 to: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 58.559
                                                                                                                                                                                                                                                                                                                              300 GluSerGluSerThrMetValTrpSerGluVal 310
                    319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTT 351
                                                           288 ysProProThrValLysAsnLeuGluGluVal.....
                                                                                  278 AG......CTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA 318
                                                                                                                              271 rGlyGluLeuGluValIleTyrAsnAlaLysGluAsnIleThrGlyLeuL 288
                                                                                                                                                               228 GTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCA 277
                                                                                                                                                                                              255 AsnīlePheGlyHisTrpAspArgThrValMetAlaLysAsnīleLysTh 271
                                                                                                                                                                                                                184 TCATIC......GATTATCAAAAAACTGGGATGGATAAATTGGATAAAATT 227
                                                                                                                                                                                                                                                             Percent Identity: 29.730
                                                                  .....Thr 299
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Swissprot_38:IL6B_HUMAN +
Swissprot_38:I12R_HUMAN +
Swissprot_38:KICH_YEAST +
Swissprot_38:CAG1_HUMAN +
Swissprot_38:CAG1_HUMAN +
Swissprot_38:GAG1_HUMAN +
Swissprot_38:S230_PLAFO +
Swissprot_38:S230_PLAFO +
Swissprot_38:YEGP_HAEIN -
Swissprot_38:YEGP_HAEIN -
Swissprot_38:YEGP_HAEIN -
Swissprot_38:YEGP_HAEIN -
Swissprot_38:YEGP_HAEIN -
Swissprot_38:YEGP_HAEIN -
Swissprot_38:YEGPO +
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Swissprot_38:FDIZ_RAT +
Swissprot_38:FDIZ_MOUSE +
Swissprot_38:FDIZ_MOUSE +
Swissprot_38:FDIZ_STRMU +
Swissprot_38:FFD_STRMU +
Swissprot_38:FFD_
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Query: US-09-2
Query length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database sequences: 83857
Database length: 30454973
Search time (sec): 45.030000
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SwissProt_38:110R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_38:KI28_YEAST
SwissProt_38:CP84_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SwissProt_38:I10R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_38:IL6B_RAT +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SwissProt_38:INGS_HUMAN
SwissProt_38:INGR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_38:INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SwissProt_3
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US-09-240-675-1_COPY_27_427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1_COPY_27_427
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AN + 692.00 1
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108.85 16.88

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114.12 17.46

112.03 18.02
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out_format :
ID INRI_HUMAN STANDA AC PIT181;
DT 01-AUG-1990 (Rel. 15, DT 01-AUG-1990 (Rel. 139, DE MINER PRON REPERON-ALPHA/BETA ON IFFBE-2000 (Rel. 139, DE MINER PRON N.A. RAY MEDLINE; 90124632.

RAY MEDLINE; 90124632.
RAY MEDLINE; 92129376.
RAY MEDLINE; 92059042.
RAY MEDLINE; 92059042.
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RAY PROSPHORYLATIC CONTACT THE SUBELON.
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SwissProt_38:YFE2_YEAST
SwissProt_38:YILI_DICDI
SwissProt_38:N153_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: SwissProt_38:INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,
RA Mullersman J., Witte M., Krishnan K., Krolewski J.;
RA Mullersman J., Witte M., Krishnan K., Krolewski J.;
RA Mullersman J., Witte M., Krishnan K., Krolewski J.;
RA Mullersman J., Witte M., Krishnan K., Krolewski J.;
RA Mullersman J., Witte M., Krolewski J.;
RT Mol. Cell. Biol. 14:8133-8142(1994).

CC -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC -!- FUNCTIONING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES,
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -!- SUBCELFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
CC -!- FUM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                EMBL; J03171; AAA52730.1;
EMBL; X60459; CAA42992.1;
PIR; A32694; A32694.
PIR; S17112; S17112.
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      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                        POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
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(See http://www.isb-sib

EMBL outstation a collaboration -

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SEQUENCE FROM N.A.

MEDLINE; 92129376.

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;

"The structure of the human interferon alpha/beta receptor gene.";

J. Biol. Chem. 267:2802-2809(1992).
                                                                                                                                                                                                                                   Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Entheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  Uze G., Lutfalla G., Gresser I.; "Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";
                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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! P43560 saccharomyces
! P36418 dictyostelium
! P49790 homo sapiens
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        INR1_BOVIN STANDARD; PRT; 560 AA. 004790; 01-004790; 01-CT-1993 (Rel. 27, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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EMBL; L06320; AAA02571.1; -
PIR; S3770; S3770;
PIR; S27387; S27387.
PFAM; PF00041; fn3; 1.
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Lim J.-K., Langer J.A.;

"Clonling and characterization of a boyine alpha interferon receptor.";

"Clonling and characterization of a boyine alpha interferon receptor.";

"Clonling and characterization of a number of profession of the function receptor for interferons alpha and beta. Binding to Type

I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BYPE INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

SUBUNITS THEMSELVES.

SUBUNITS THEMSELVES.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

Mouchel-orantiviral activities of the human alpha inte

determined at the level of receptor (IFNAR) structure.

FEBS Lett. 313:255-259(1992).
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 103

gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA

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seq_name: SwissProt_38:INR1_SHEEP
HAN C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

"Molecular cloning of ovine and bovine type I interferon receptor

"I subunits from uteri, and endometrial expression of messenger

"I subunits from uteri, and endometrial expression of messenger

"I ribonucleic acid for ovine receptors during the estrous cycle and

"I regnancy.";

"I endocrinology 138:4757-4767(1997).

"I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYP

"I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYP

"I FUNCTION: TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

"I RILUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

"SUBUNITS THEMSELYES."

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"I SUBCELLULLAR LOCATION: TYPE I MEMBRANE PROTEIN.

"I SUBCELLULLAR LOCATION: TYPE I MEMBRANE PROTEIN.

"I TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT

CONCEPTUS AT DAY 15 OF PREGNANCY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euraryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERCERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
(INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                       MEDLINE; 98006426.
Han C.-S., Mathial
                                                                                                                                                                                                                                                                                                                endometrium.";
J. Mol. Endocrinol.
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MEDLINE; 97135690.
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                                                                                                                                                                                                                                   4
           CCAAATGCAACTTTTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT
                                         uGlyThrAspAsnTrpLysLysLeuProGlyCysGlnH1sIleThrSerS
                                                                                                                                                AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                  gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLysSer...GluA
                                                                                                                                                                                        ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA
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                                                             TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                 SerSerGluSerValArgAsnValThrPheSerAlaAspTyrGlnIleLe
                                                                                            AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC
                                                                                                                           snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                             erLysCysAsnPheSerSerValGluLeuLysAspValPheGluLysIle
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1 24 BY SIMILARITY.
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-> D (IN REF. 2).
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seq_name: SwissProt_38:INR1_MOUSE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
"Behavior of a cloned murine interferon alpha/beta receptor exp.
in homospecific or heterospecific bactond.";
in homospecific Sci. U.S.A. 89:4774-4778(1992).
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROINCIDING JAKS, TYK, STAT PROTEINS AND IFN-R ALPHA-AND BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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MGI:107658;
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                                                                                                                                                                                                                              Transmembrane;
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                          POTENTIAL.
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POTENTIAL.
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BY SIMILARITY.
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7EC6DFF370185D3A CRC64;
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Mus.
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O BETA-
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
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neighbor.";
J. MOL. Evol. 41:338-344(1995).

J. WOL. Evol. 41:338-344(1995).

J. FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.

J. SUBCELIULAR LOCATION: TYPE I MEMBRANE PROTEIN.

J. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

J. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RE
                                                                                                           SEQUENCE FROM N.A. MEDLINE; 96054036. Lutfalla G., McInnis
                                                                                                                                                                                                                          TISSUE-FETAL BRAIN;
MEDLINE; 93300510.
Lutfalla G., Gardiner K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
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                                                                                                                                                                            "A new member of the cytokine receptor gene family maps on chromosome 21 at less than 35 kb from IFNAR."; Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                            nomo saprens (nomman).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRF4_HUMAN
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                                                                                               "Structure of the human
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                                                                                               CRFB4 gene:
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Quality:
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Percent Similarity:
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381 GATTGGTCCTCCA 393
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                                                                    ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
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                                                                                                                                                                                                                                                                                                                                                                                              yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
                                 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                       erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy
                                                                                                                                                                            sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
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Gaps: 5
Percent Identity: 33.058
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A -> D (IN REF. 2).

FUGHP -> VGRME (IN REF. 2).

MISSING (IN REF. 2).

M: 66706C79F8514B23 CRC64;
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EXTRACELLULAR (POTENTIAL).
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Seq_documentation_block:
ID INGS_HUMAN STANDA
AC P348484
DT 01-OCT-1994 (Rel. 30,
DT 01-OCT-1997 (Rel. 35,
DE RIVERSON SEPIENS (HUMAN)
CC ENTARTS: 94170380.
RA HOMO SEPIENS FROM N.A.
RC TISSUE-LUNG FIRROBLAS
RX MEDLINE; 94170380.
RA WANG N., Emanuel S.L.
RA WANG N., Emanuel S.L.
RA WANG N., Emanuel S.L.
RT "Identification and sactivation of the hum
RL Cell 76:793-802(1994)
CC -!- SUBCELLULAR LOCAT
CC SIGNAL THE FRANSDUCTI
CC INTERACT WITH GAR
CC -!- SUBCELLULAR LOCAT
alignment_block:
US-09-240-675-1_COPY_27_427 x INGS_HUMAN
                                                                                                                                                                                    alignment_scores
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                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1997 (Rel. 35, Last annotation update)
1NTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.; "Identification and sequence of an accessory factor required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U05875; AAA16955.1; -. EMBL; U05877; AAA16956.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LUNG FIBROBLAST;
MEDLINE; 94170380.
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                                                                                                                                                         Quality:
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1.393
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                                                                                                   Percent Identity:
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18C61B10AD90E509 CRC64;
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Align seg 1/1 to: INGS\_HUMAN

from: 1 to:

337

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34 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA...

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seq_name: SwissProt_38:INGR_HUMAN
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gar "Alignment of disulfide bonds of the extracellular domain interferon gamma receptor and investigation of their role biological activity.":
Biochemistry 32:2423-2430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            Zauodny P.J., Narula S.K.;
"Crystal structure of a complex between soluble high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                          MEDLINE; 95342235.
Walter M.R., Windsor W.T., Nagabhushan T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aguet M., Dembic Z., Merlin G.;
"Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE: 89003065.
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MEDLINE;
                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF
                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF
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                         COMPLEX WITH ANTIBODY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex."; J. MOL. Biol. 273:882-897(1997).
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PIR; ?
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-!- PIM: PHOSPHORYLARED AT SER/THR RESIDUES.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sogabe S., Stuart F., Henke Winkler F.K., Robinson J.A.;
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                         AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA
                                                                                       AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                 MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
                                                                                                                                                                                                            GTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATG
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                                                           snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr
                                                                                                                      aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA
                                                                                                                                                   GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
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.GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; Signal; Phosphorylation
                                                                                                                                                                                                                                            to: INGR_HUMAN from: 1
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CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERFERON-GAMMA RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                              to: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saiz J.E., Buitrago M.J., Garcia R., Revuelta J.L., del Rey F "The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevisiae chromosome IV contains the KIN28, MS: PHO2, POL3 and DUN1 genes, and six new open reading frames."; Yeast 12:1077-1084(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIN28 OR YDL108W OR D2330.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
SERINE/THREONINE-PROTEIN KINASE KIN28 (EC 2
EMBL; X04423; CAA28019.1; -. EMBL; X95644; CAA64904.1; -. EMBL; Z74156; CAA98675.1; -. PIR; A25698; A25698.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: PROTEIN KINASE ESSENTIAL FOR CELL PROLIFERATION.
FUNCTION IN ASSOCIATION WITH CYCLIN CCL1.
-!- SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. Biol. 234:307-310(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valay J.G., Simon M., Faye G.; "The kin28 protein kinase is associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / FY1679;
MEDLINE; 97051597.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 87053839.
Simon M., Seraphin B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATTGCGTATAAGAGCA...........GAAAAGAAAACACTTCTTCATG
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(EC 2.7.1.-).
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seq_documentation_block:
ID CP84_ARATH STANDA
AC 042600;
DT 15-DEC-1998 (Rel. 37,
DE CYTOCHROME P450 84A1
GN CYP84A1 OR FAH1 OR F20
OS Arabidopsis thaliana
OC Eukaryota; Viridiplan
OC euphyllophytes; Sperm
OC core eudicots; Rosida
OC arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE; 96293440.
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Quality:
Ratio:
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US-09-240-675-1_COPY_27_427 x
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                                                                    Q4260;
Q4260;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 84A1 (FERULATE-5-HYDROXYLASE) (EC 1.14.---) (F5H).
CYP84A1 OR FAH1 OR F23E13.110.
CYP84A1 OR FAH1 OR F23E13.110.
Arabidopsis thallana (Mouse ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyliophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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TRANSFAC; T0219
SGD; L0000905;
PROSITE; PS0010
PROSITE; PS0010
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BINDING
ACT_SITE
SEQUENCE
   SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA; MEDLINE; 96293440.
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
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AIN 7
BIND 13
DING 36
DING 129
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
GW; 763A5720A1D9ACF3 CRC64;
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Gaps:
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alignment_scores:
Quality:
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US-09-240-675-1_COPY_27_427 x CP84_ARATH
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PROSITE: P500086; CYTOCHROME_P450;
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Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Dy
Hohelsel J., Jesse T., Heijnen L., Vos P., Mewes H.-W.,
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BINDING 458 458 HEME (BY SIMILARITY).
SEQUENCE 520 AA; 58720 MW; E812779AF5BF01BC CRC64;
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eIleProLysLysSerArgValMetIleAsnAlaPheAlaIleGlyArgA
                                                                                                                                     ProLeuLeuHisGluThrAlaGluAspThrSerIleAspGlyPhePh
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Seq_documentation_block:
ID 116B_RAT STANDARD;
AC P40190;
DT 01-FEB-1995 (Rel. 31, Last
DT 11-JUL-1999 (Rel. 38, Last
DT 15-JUL-1999 (Rel. 38, Last
DT 15-JUL-1999 (Rel. 38, Last
DE 15-JUL-199 (Rel. 38, La
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PIR; A44257; A44257.
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          SER-RICH.
BY SIMILA
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              SIMILARITY
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Transducing molecule, gp130.";

It fansducing molecule, gp130.";

It Genomics 14:666-672(1992).

C -!-FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR C. IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-61-16. ALPHA CHAIN) COMPLEX, CRESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, CAND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN C. EMBRYONIC DEVELOPMENT (BY SIMILARITY).

C -!- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SINGLELIAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SINGLARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

C -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-FEB-1995 (Rel. 31, LAST Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
5 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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lon of the rat liver IL-6 signal
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ID I10R_HUMAN STAN
                          seq_name: SwissProt_38:I10R_HUMAN
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                                                               AGCTCAGATT 384
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                                                                                                                                                                            ProArgThrSerPheThrValGlnAspLeuLysProPheThrGluTyrVa 295
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                                                                                                                     rpSerGluGluAlaSerGlyThrThrTyrGluAspArgProSerLysAla 328
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alignment_block:
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
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DOMAIN
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MEDILINE; 94165477.

Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;

"Expression cloning and characterization of a human IL-10 receptor.

J. Immunol. 152:1821-1829(1994).

J. Immunol. 152:1821-1829(1994).

J. IMMUNOL. RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PEMC. FAINT EXPRESSION
IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENT
LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO sapiens (Human).
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Entheria; Primates; Catarrhini; Hominidae; Homo.
                                              104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL10RA OR IL10R.
                                                                                            19
                                                                                                                                     54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 103
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                                                                                                                                                                                                                                    4 ATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
erValTrpPheGluAlaGluPhePheHisHisIleLeuHisTrpThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                    LeuValValLeuLeuAlaAla.....LeuLeuSerLeuArgLeuGly..
                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
236
257
202
74
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1.026
58.915
                                                                                            .SerAspAlaHisGlyThrGluLeuProSerProProS
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62903
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ME.
                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                   from: 1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Gaps:
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                                                                                                                                                                                                                                                                                   578
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6
24.031
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154

AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC: 203

Quality:

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seq_name: SwissProt_38:6DCS_SOYBN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
01-AUG-1992 (Rel. 26, Last annotation update)
NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254
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                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Induced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis of phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63)."; Eur. J. Biochem. 196:423-430(1991).

-i- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF 4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF GLYCEOLLIN TYPE PHYTOALEXINS.

-i- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max (Soybean)
    PFAM; PF00248; aldo_ket_red; 1.
Flavonoid biosynthesis; Oxidoreductase; NADP.
SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
                                                            PRINTS; PR00069; ALDKETRDTASE
PROSITE; PS00062; ALDKETO_REDUCTASE_2;
PROSITE; PS00063; ALDKETO_REDUCTASE_3;
PROSITE; PS00798; ALDKETO_REDUCTASE_1;
                                                                                                                                                                  EMBL; X55730; CAA39261.1; -. PIR; S14222; S14222.
                                                                                                                                                                                                                                                                                                                                                                                              -1- INDUCTION: BY PATHOGEN ATTACK.
-1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleProAsnGlnSerGluSerThrCysTyrGluValAlaLeuLeuArgTy 64
                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHYTOALEXINS IN SOYBEAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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alignment\_scores:

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alignment_block:
seq_name: SwissProt_38:I10R_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O61727:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214
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                                                                                                                                                                                                 MEDLINE; 94068585.

HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;

"A receptor for interleukin 10 is related to interferon receptors.";

Proc. Natl Acad. Sci. U.S.A. 90:11267-11271(1993).

-I- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.

-I- SUBCELULUAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 LysSerLeuLysThrLeuGlnLeuGluTyrLeuAspLeu.......
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL10RA OR IL10R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 aPheSerProLeuArgLysGlyAlaSerArgGlyProAsnGluVal
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
           alignment_block:
US-09-240-675-1_COPY_27_427 x
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CARBOHYD
SEQUENCE
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CARBOHYD
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DOMAIN
                                                                                                                                           documentation_block:
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SIGNAL
                                           P40189;
p40189;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA)
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130)
RECEPTOR) (CDW130) (CD130 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD;
                                                                                                                                                                                             121 eThr 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 TCCTGAGGTGG.....AACAGGAGCGATGAGTCTGTCGGGAAT
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                     Homo sapiens
                                   IL6ST.
                                                                                                                                 IL6B_HUMAN
                                                                                                                                                                                                                                           105 AlaValAspAsnSerGlnTyrSerAsnTrpThrThrThrGluThrArgPh
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                                                                                                                                                                                                                                                                                                                   TCAAGCTGAATGTTTATGAAGAA.....ATTAAATTGCGTATAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uLeuProSerProSerTyrValTrpPheGluAlaArgPhePheGlnHisI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuValThrIleSerSerLeuSerLeuGluPheIleAlaTyrGlyThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #GI:96538;
                                                                                                                                                                     SwissProt_38: IL6B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                  GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCA...TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
263
204
50
66
113
182
238
575
           Metazoa;
(Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA16156.1; -.
                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL10RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.50
1.062
61.017
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64248
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241
262
262
575
225
50
66
113
113
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POTENTIAL.
INTERLEUKIN-10 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I10R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
           Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575
           Vertebrata; Mammalia
                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
5
23.729
                                                                                                                                                                                                                                                                                                                   315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                      (INTERLEUKIN
                                                         (ONCOSTATIN
           A Bravo J. Staunton D., Heath J.K., Jones E.Y.;

A Proposed structure of a cytokine-binding region of gp130.*;

EMBO J. 17:1665-1674(1998)

C -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6. LIF, OSM, CNTF, AND IL-11 CAN UTILIZE Gp130 FOR INITIATING C SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN C EMBRYONIC DEVELOPMENT (BY SIMILARITY).

C -1- SUBGUNIT: HETTERODIMER OF AN ALPHA AND A BETA CHAIN.

C -1- SUBGURIT: HETTERODIMER OF AN ALPHA AND A BETA CHAIN.

C -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.

C -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE CZ-TYVED DOMAINS.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

WHW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cdd30.htm".
                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                          DOMAIN
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 9
                    CARBOHYD
CARBOHYD
                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                    Receptor;
Repeat; 3:
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-MYELOMA, AND PI
MEDLINE; 91084844.
Hibi M., Murakami M.,
                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Butheria; Primates; Catarrhini; Hominidae; Homo
[1]
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M57230; AAA59155.1; -. PIR; A36337; A36337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00340; RECEPTOR_CYTOKINES_2; PFAM; PF00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63:1149-1157(1990).
                                                                                                                                                                                                                                                                                                                    3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98169383.
                                                                                                                                                                                                                                                                                                                               Transmembrane;
       564
918
                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning and
          ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND PLACENTA;
                                  103522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
                                                                                                                                                                                                                                                                                                                               Glycoprotein;
          ¥.
                                                                                                                                                                            IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                             POTENTIAL.
INTERLEUKIN-6
EXTRACELLULAR
                    POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                   SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirano T., Taga T., Kishimoto T
on of an IL-6 signal transducer,
          D813F3672DD10D53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 122-325
                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain;
                                                                                                                                                                                                                                                                                          RECEPTOR BETA CHAIN.
                                                                                                                                                                                                                                                                               (POTENTIAL)
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seq_documentation_block:
ID I12r_HUMAN STANDA
AC P42701:
DT 01-NOV-1995 (Rel. 32,
DT 01-NOV-1995 (Rel. 32,
DT 15-JUL-1999 (Rel. 38,
DE INTERLEUKIN-12 RECEPT
GN IL12RB OR IL12RB OR
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; C
CC Eutheria; Primates; C
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94267217.
RA Chua A.O., Chizzonite
RA Gubler U;
RT "Expression cloning of the cytokine recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_27_427 x
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                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: SwissProt_38:I12R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 SerThrValTyrPheValAsnIleGluValTrpValGluAlaGluAsnAl
                                                            SEQUENCE FROM N.A.
MEDLINE; 94267217.
Chua A.O., Chizzonite R., De
Minetti L.J., Warrier R.R.,
                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN PRECURSOR
IL12RB1 OR IL12RB OR IL12R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302
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                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              336 IleAsp 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
    "Expression cloning of a human IL-12 receptor component. A new member of the cytokine receptor superfamily with strong homology to gp130.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerSerIleLeuLysLeuThrTrpThrAsnProSerIleLysSerValIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aLeuGlyLysValThrSerAspHisIleAsnPheAspProValTyrLysV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTGGAAAA......AATCTAAAATCTCCTCAAAAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAGAAAAC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erGlnIleProPro...GluAspThrAlaSerThrArgSerSerPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eIleLeuLysTyrAsnIleGlnTyrArgThrLysAspAlaSerThrTrpS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alLysProAsnProProHisAsnLeuSerValIleAsnSerGluGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyIleThrTyrGluAspArgProSerLysAlaProSerPheTrpTyrLys 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tLysGluAspGlyLysGlyTyrTrpSerAspTrpSerGluGluAlaSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ACTTCTTCATGGTATGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
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                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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1.077
46.711
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Percent Identity:
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                                                              Desai B.B., Tru
., Presky D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to:
                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                 662
                                                              Truitt T.P.,
H., Levine J.
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6
21.711
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                                                                J.F.,
                                                                                   Nunes
                                                                Gately M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270
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alignment_block:
US-09-240-675-1_COPY_27_427 x I12R_HUMAN
                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                     Align seg 1/1 to: I12R_HUMAN
                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECOND PROTEIN 2 AMINO ACIDS SHORTER.
-I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-I- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                     107 ValLeuTyrThrValThrLeuTrpValGluSerTrpAlaArg...AsnGl 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U03187; AAA21340.1; -.
MIM; 601604; -.
  183
                          156
                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                84 AAATCTAAAATCTCCTCAA.....
                                                                                                                                                                                                34 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAA
                      ArgMetGluTrpGluThrProAspAsnGlnValGlyAlaGluValGlnPh
                                                                                                                     nThrGluLysSerProGluValThrLeuGlnLeuTyrAsnSerValLysT
TTCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTG
                                                ATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG...AATGTGACTTT
                                                                                             yrGluProProLeuGlyAspIleLysValSerLysLeuAlaGlyGlnLeu
                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                                                                                                                                                                                  75.50
1.020
52.857
                                                                                                                                                                                                                                                                                                                                                         442
456
662
73108
                                                                                                                                                                                                                                                                                                                                                                                                        34444
3459
34444
3449
                                                                                                                                                                                                                                                                                                                                                         MW.
                                                                                                                                                                                                                        from: 1 to:
                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
KAKM -> DE
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                        NKM -> DE (IN A SHORTER FORM).
541ADA60F62DA1EF CRC64;
                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                        662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                    27.143
                                                                                                                                                                                                                                                                                                           140
                                                                           155
                                                                                                                           139
                                                                                                                                                  102
                                                   182
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sp_nammal:018966
sp_plant:09%FM2
sp_rodent:007313
sp_rodent:007313
sp_rodent:007280
sp_rodent:007311
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Query: US-09-240-675-1_COPY_27_427
Query length: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_invertebrate:045604
sp_virus:065525 +
sp_fung1:008773 +
                                sp_virus:039225
sp_invertebrate:002424 +
sp_invertebrate:023047 +
sp_bacteria:034739 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database sequences: 225878
Database length: 69334122
Search time (sec): 89.9400
                                                                                                                                                             sp_invertebrate:061210
                                                                                                                                                                                       sp_invertebrate:Q25994
sp_plant:Q9ZQ67 +
                                                                                                                                                                                                                                                    sp_rodent:007310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:076835
sp_mammal:018965 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_bacteria:085940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:Q18876
sp_plant:Q41577 +
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sp_plant:Q39688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_invertebrate:076514 + sp_human:09Y5T6 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_mamma1:028733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_invertebrate:Q20930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_fung1:Q06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:Q10466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_vertebrate:013048 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_invertebrate:Q23020 +
sp_invertebrate:Q23550 +
sp_invertebrate:Q23551 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_human:Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_vertebrate:Q9YGC8 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent: Q63953
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Sequence
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-Q-/cgn2_1/USPTO_spool/USO9240675/runat_30052000_164313_24664/app_query.fasta.l
-DB-SPTREMBL_12 -QFMT-fastan -SUFFIX-modif.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINANTCH=0.100 -LOOPEL-0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -XGAPEXT=0.500
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-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-PCt
-ALIGN-15 -MODE-LOCAL -OUTFMT-PIS -NORM-ext -MINLEN-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-240-675-1_COPY_27_427
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1W0 + 248.50

+ 127.00

+ 120.00

108 + 104.50

108 + 104.50
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   + 70.00 110.50 10.60

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69.50 113.69 12.09

69.50 106.72 12.06

+ 69.00 125.18 13.84

68.50 122.75 15.76

68.50 121.80 15.75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 | Q9yhw0 gallus gallus (chicken).

349 | Q61190 mus musculus (mouse). cy

332 | Q63953 mus musculus (mouse). in

341 | Q9ygc8 gallus gallus (chicken).

484 | Q14936 homo sapiens (human). in

486 | Q23020 caenorhabditis elegan

487 | G048 | Q23551 caenorhabditis elegan

488 | Q33521 caenorhabditis elegan

489 | Q33551 caenorhabditis elegan

480 | Q33551 caenorhabditis elegan

480 | Q33551 caenorhabditis elegan

480 | Q33648 xenopus laevis (african

480 | Q35614 xenopus laevis (elegan

481 | Q6349 saccharomyces cerevisiae

482 | Q6349 saccharomyces cerevisiae

483 | Q654504 caenorhabditis elegan

583 | Q45604 caenorhabditis elegan

585 | Q2873 saccharomyces cerevisiae

486 | Q3930 caenorhabditis elegan

5875 | Q3930 caenorhabditis elegan

5875 | Q39586 daucus carota (carrot).

486 | Q39686 daucus carota (carrot).

4876 | Q39686 caenorhabditis elegans

488 | Q39688 daucus carota (carrot).
      426
3168 :
368 :
960 :
987 :
1395 :
1399 :
1399 :
1438 :
1438 :
14470 :
365 :
365 :
365 :
                                                                                                                                                                             1 085940 sphingomonas aromaticivo (1076835 caenorhabditis elegans (108965 bos taurus (bovine). eag (108966 bos taurus (bovine). eag (108967 arattus norvegicus (rat) (107313 rattus norvegicus (rat) (107313 rattus norvegicus (rat) (107312 rattus norvegicus (1
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5 | O61210 caenorhabditis elegan

1 O39225 murine hepatitis virus

1 O02424 caenorhabditis elegans

1 O23047 caenorhabditis elegans

1 O23047 bacillus subtilis. ykba

1 O23552 caenorhabditis elegans
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   seq_name:
                                                                   124
                                                                                                                             351
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sp_plant:023357
sp_plant:Q41442
sp_plant:Q39658
sp_vertebrate:Q9W669
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-240-675-1_COPY_27_427
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01-MAY-1999 (TrEMBLrel. 10, Creat.
01-MAY-1999 (TrEMBLrel. 10, Last
01-MAY-1999 (TrEMBLrel. 10, Last
INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 0:0-0(1999).
EMBL; AF082664; AAD13669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparative genomic analysis receptor gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                    TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                                                                                                                                                                               GGGAATGTGACTTTTTCATTCGATTATCAA......AAAAC
                                                                                                                                                                                                                                                                                                     Ratio:
Similarity:
                                                                                                                            CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA
                                                                                                                                                                                                                                                                                      laValAsnThrAsnPheThrLeuMetTrpAsnTyrThrGlyAspGlyThr
                                                                                                                                                                                                                                                                                                                                              sCysAlaGlyGlnThrAsnLeuLysSerProGlnAspIleGlnValTyrA
                                                                                                                                                                                                                                                                                                                                                                           AGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACA
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TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA
                                                        TTGCGTATAAGAGCAGAA....AAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                        rSerGluProGluTrpLysGluLeuSerGlyCysGlnAsnValSerHisT
                                                                                                                                                                                                                               ...AsnValThrPheSerAlaGlnTyrGlnCysPheAspAspLeuGlnTh
                                                                                                               hrGluCysAspPheSerSerAlaIleThrAlaTyrTyrAspThrHisHis
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Last annotation update)
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interferon/interleukin-10
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Q41442
Q39658
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2 solanum tuberosum
8 cucumis sativus (C)
9 carassius auratus
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SOO SOOR THE TRACE OF THE TRACE
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US-09-240-675-1_COPY_27_427 x Q61190
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seq_name: sp_rodent:Q63953
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Q61190;
Q61190;
Q1-NOV-1996 (TIEMBLrel. 01, Created)
Q1-NOV-1996 (TIEMBLrel. 02, Last sequence update)
Q1-NOV-1999 (TIEMBLREL. 12, Last annotation update)
Q1-NOV-1999 (TIEMBLREL. 12, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
ILIORB OR CRED4 OR CREZ-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIBBS V.C., PENNICA D.;
"CRF2-4: isolation of cDNA clones_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
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                                                                                                                                                                                                                                                                                                         387 TCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 GGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGlnT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 GTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sargThrAlaSerThrGlnCysAspPheSer.....HisLeuSerLysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluSerTyrArgSerPheGlnAspHis......CysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA....AAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAACACTTCT
                                                                                                                                                                                                                                          yProProGluMet 118
                                                                                                                                                                                                                                                                                                                                                                           GluTrpValAsnVal...ThrPheCysProValGluAspThrIleIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrGlyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127.00
1.693
61.983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 30.
      Created)
                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding the human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                         332
                                                                            B
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Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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alignment_block:
US-09-240-675-1_COPY_27_427 x Q63953
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Quality:
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A PESTRA S., DEMBIC Z.;

IT "Genomic organization and promoter analysis of the gene lfngr2
IT encoding the second chain of the mouse interferon-gamma receptor.";

IZ Scand. J. Immunol. 44:599-606(1996).

REMBL; U69599; AAC52938.1;

REMBL; U69599; AAC52938.1;

REMBL; U69595; AAC52938.1; JOINED.

REMBL; U69596; AAC52938.1; JOINED.

REMBL; U69597; AAC52938.1; JOINED.

REMBL; U69596; AAC52938.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: Q63953 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129SV/J;
MEDLINE; 97128072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 94170381.
HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
"A novel member of the interferon receptor family complements
"A novel member of the murine interferon gamma receptor in human
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (Trembirel. 01, Last sequence update)
01-NOV-1999 (Trembirel. 12, Last annotation update)
INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 76:803-810(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFNGR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBENSPERGER C.,
                                                                        310 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                        228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 ACAGGAGCGATGAGTCT......GTCGGGAATGTGACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LeuGlyAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TTGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCCC
                                                                                                                                                                                                                                                                                                                                         G.....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
| :::||| :::::::
uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
:::||||||:::::: ||| ||||||:::|||
ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                       lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                        luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120.00
1.500
61.538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 8
Percent Identity: 30.769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332
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                                                                                                                                                                                                                                                                                                                                                       93
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357 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396

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alignment_block:
US-09-240-675-1_COPY_27_427 x Q9YGC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_vertebrate:Q9YGC8
seq_documentation_block:
ID Q14936 PRELIMI
AC Q14936;
                                                                seq_name: sp_human:Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9YGC8 from: 1 to: 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 GAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGAT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1; -.
EMBL: AF082666; AAD13671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REBOUL J., GARDINER K., MONNERON D., "Comparative genomic analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
INTERLEUKIN-10 RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                           100
                                                                                                                                                                                                                                                                              285
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                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTG 146
                                                                                                     GlyProProSerVal 121
                                                                                                                                                                                                        CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATT 384
                                                                                                                                                                                                                                        TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT 334
:|||||
rvalTyrGlyAlaTyrValLeuArgValArgThrGluTrpGluAspGluH 100
                                                                                                                                                                                                                                                                                                                                                                                                                    ....TATCAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                      pAspProProGlyValArgLysGlyAsnLeuSerTyrThrValGlnAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProArgAsnAlaArgIleSerSerValAsnPheArgSerValLeuLeuTr 40
                                                                                                                                                                       isSerAspTrpAlaValValArgPheLysProMetAlaAspThrValIle
                                                                                                                                                                                                                                                                                                                                               TGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAA 284
                                                                                                                                                                                                                                                                                                                                                                               ysSerIlePheProLysGlnAsnPheAsnAsn......val 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oPheGlnHisTyrGluAsnValThrValGlyProProLys 139
                                                                                                                                                                                                                                                                                                             ThrThrAsnLeuAsnValThrGluCysAspValSerSer....LeuSe
                                                                                                                                     GGTCCTCCAGAAGTA 399
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA;
                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104.50
1.713
58.095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 105
Gaps: 3
Percent Identity: 27.619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341
                  484
                  ⋧
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192
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SQRRRLL RAP PLAR RAP PROPERTY AND CONTRACT OF THE CONTRACT OF 
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US-09-240-675-1_COPY_27_427 x Q14936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1994) to the EMBL/Ge EMBL; U19247; AAC52064.1; JOINED. EMBL; U19241; AAC52064.1; JOINED. EMBL; U19242; AAC52064.1; JOINED. EMBL; U19243; AAC52064.1; JOINED. EMBL; U19244; AAC52064.1; JOINED. EMBL; U19244; AAC52064.1; JOINED. EMBL; U19245; AAC52064.1; JOINED. EMBL; U19245; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL. 08, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEMBIC Z.;
"The gene for the ligand binding chain receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERLIN G., VAN DER LEEDE B.-J.M., MCKUNE K., KNEZEVIC N., BANNWARTH W., ROMQUIN N., VIEGAS-PEQUIGNOT E., KIEFER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE FROM N.A. MEDLINE; 97246734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 89003065.
AGUET M., DEMBIC Z., MERLIN G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 45:413-421(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG
                                                                                                                                                                                                                                                                                                      AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATG
                                                                       isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                               GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
                                                                                                                                                                                                                          nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH
                                                                                                                                                                                                                                                                                                                                                                                  .....GlnIleMetProGlnValProValPheThrValGluValLysAs
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1.018
61.765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBC99D1F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the human interferon-gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136
5
24.265
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                                                                           86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma
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SER REPRESENTATE PROPERTIES OF SERVICE CONTRACTOR S
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                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_27_427 x Q23020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                      Align seg 1/1 to: Q23020 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; X15423; CAA33463.1; ".

R EMBL; Z73899; CAA98081.1; ALT_INIT.

R EMBL; Z73897; CAA98081.1; JOINED.

R HSSP; Q63450; 1A06.

R PFAM; PF00041; fn3; 31.

R PFAM; PF00041; fn3; 31.

R PFAM; PF00069; pkinase; 1.

R PFAM; PR00014; FNTYPEIII.

R PFAM; PR00014; FNTYPEIII.

N MYOSIN; KInase; 668449 MW; 1977C602 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
                                                                                                                             1073
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BENIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
"Additional sequence complexity in the muscle gene, unc-22, encoded protein, twitchin, of Caenorhabditis elegans.";
Genetics 134:1097-1104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 93387664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BENIAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G., WATERSON "Sequence of an unusually large protein implicated in regulati myosin activity in C. elegans.";
Nature 342:45-50(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNC-22 OR ZK617.1.
                              123 AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172 :::::|||||||::: ||| |||::: ||||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE; 90044042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HARRIS B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roLysLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpValArgValLysAlaArgValGlyGlnLysGlu....SerAlaTy
                                                                                                                      CTAAAATCTCCTCAAAAA......GTAGAGGTC...GACATCAT 122
eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 26.496
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Last sequence update)
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Gaps:
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seq_documentation_block:
ID Q23550
AC Q23550;
AC Q23550;
DT 01-NOV-1996 (TIEMBLTel. 01.
DT 01-NOV-1998 (TIEMBLTel. 12.
DE UNC-22 PROTEIN.
GN UNC-22.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoo
OC Rhabditina; Rhabditoidea; I
RN [1]
RP SEQUENCE FROM N. A.
RA WHITE S.;
RA WHITE S.;
RA WHITE S.;
RA SEMBL; Z73897; CAA98064.1; CAR98064.1; DR EMBL; Z73897; CAA98064.1; DR PFAM; PFO00041; fin3; 31.
DR PFAM; PFO00041; FINA.
DR PFAM; PFO00047; PRIVABELII
DR PRINTS; PRO0014; FINTYPEIII
SQ SEQUENCE 6831 AA; 75257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_invertebrate:Q23550
                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_427 x Q23550
                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1777, EMBL; 273897; CAA98064.1; JOINED. EMBL; 273897; CAA98064.1; JOINED. EMBL; 273899; CAA98064.1; JOINED. EMBL; 273899; CAA98064.1; JOINED. ENS. PEAM; PFO0041; FN3; 31. PFAM; PF00047; 19; 17. R PFAM; PF00069; PKINASE; 1. R PRINTS; PRO0014; FNTYDEIII. R PRINTS; PRO0014; FNTYDEIII.
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                                                                                             1872
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                                                                                                                                                                                 1856 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh 1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                       CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpValPro......CysAlaLysValLysAspThrLysAlaHisIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTGACTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                                 AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172
luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg
                                        ATGTGACTTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                           eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                            to: Q23550 from: 1 to: 6831
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1.151
62.393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                             : 117
: 8
: 26.496
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       1905
                                                                                             1889
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seq_name: sp_invertebrate:Q23551
             Quality:
Ratio:
Percent Similarity:
                                                                                                                    Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases:
EMBL; 273899; CAA98082.1; -.

REMBL; 273897; CAA98082.1; JOINED.
EMBL; 273897; CAA98065.1; -.

EMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

RESSP; PC00241; IFNA.

RESSP; PC00241; IFNA.

REAM; PF00047; 19; 17.

REAM; PF00069; Pkinase; 1.

REMINTS; PR00014; FNTYPEIII.

REMINTS; PR00014; FNTYPEIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 1967
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                                                                                                                                                                                                                                                                                                                                                                                        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., KEMEN T., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Ehabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZK617.1B PROTEIN.
ZK617.1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HARRIS B.;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. WHITE S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eAspGlyLeuLysLysGly......GlnThrTyrGlnPheArgValLysA 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpValPro.....CysAlaLysValLysAspThrLysAlaHisil 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
             84.00
1.151
62.393
eaps: 8
Percent Identity: 26.496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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alignment_block:
US-09-240-675-1_COPY_27_427 x Q23551
SSE SECTION OF SECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: sp_vertebrate:013048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: Q23551 from: 1 to: 7160
                                                          EMBL; U79162; AAC60127.1; -.
HSSP; P18075; IBMP.
PROSITE; PS00250; TGF_BETA; 1
PFAM; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
O13048 PRELIMINARY; PRT; 402 AA.
O13048;
O1-JUL-1997 (TIEMBLIEL 04, Created)
O1-JUL-1997 (TIEMBLIEL 04, Last sequence update)
O1-NOV-1999 (TIEMBLIEL 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2185 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2218 luProlleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XNR4
Glycoprotein
SEQUENCE 40
                                                                                                                                                                                                                                                           Dev. Biol. 184:367-372(1997).
                                                                                                                                                                                                                                                                                                                                     organizer.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97278865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XNR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 CTAAAATCTCCTCAAAAA......GTAGAGGTC...GACATCAT 122
                                                                                                                                                                                                                                                                                                                                                                                                      JOSEPH E.M., MELTON D.A.;
                                                                                                                                                                                                                                                                                                                                                                'Xnr4: a Xenopus nodal-related gene expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTGACTITTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr
   402 AA; 46271 MW;
   039E7186 CRC32;
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                                                                                                                                                                                                                                                               THE TGF-BETA FAMILY
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                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                               Spemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2279
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alignment\_scores:

Quality: Ratio:

80.00 1.404 50.893

Gaps: Percent Identity:

23.214

Percent Similarity:

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seq_documentation_block:
ID Q10466
PRELIMINA
AC Q10466;
DT Q1-NOV-1996 (TrEMBLre
DT Q1-NOV-1999 (TrEMBLre
DT Q1-TISUE-HEART:
RN GEDLENE; 96026330.
RA LABEIT S., KOLMER B.;
RT G13SUE-HEART:
RN G2918 (19.3)
RN G2918 (29.3)
RN GDLINE; 96026330.
RA LABEIT S., GAUTEL M.,
RT "TOWARDS a molecular
RL EMBO J. 11:1711-1716(
RN [3]
RP SEQUENCE OF 1976-2014
RA LABEIT S.;
SUBMITTED M., CASTIGLION
RA GAUTEL M., CASTIGLION
RT "A CALMODULIN BIN AND IN N
CC -1-FUNCTION: THIS G3
CC -1-FUNCTION: THIS G3
CC -1-FUNCTION: THIS G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name:
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US-09-240-675-1_COPY_27_427 x 013048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            010466;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN
Homo sapiens (Human).
                                                                                                                                                                                                                                                                     SEQUENCE OF 22277-25376 FROM N.A. MEDLINE; 92258380.

LABEIT S., GAUTEL M., LAKEY A., TRI "Towards a molecular understanding EMBO J. 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
                                                            MEDLINE; 95331314.

GAUTEL M., CASTIGLIONE-MORELLI M.A., F
"A calmodulin-binding sequence in the titin kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96026330.
LABEIT S., KOLMER B.;
                                                                                                                                                                                         Submitted (DEC-1994)
                                                                                                                                                                                                              SEQUENCE OF 1976-2014 FROM N.A. LABEIT S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 eLysGluHisValMetGlyMetLysHis.....valProProA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          "Titins: giant proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                   ience 270:293-296(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nHisAlaTyrMetGlnSerLeuLeuAsnTyrTyr 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysGluGlyGluCysProSerProValAsnGluSerValLysProAsnAs
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    FUNCTION: THIS GIANT MUSCLE ASSEMBLY AND IN MAINTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eLysGlnIleGlyTrpAspSerTrpIle.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAGCAGAAAAAGAAAACACTTCTTCATGGTAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTAT...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 402
                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                          charge of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
    PROTEIN MAY BE
                                                                                                                                                                                                                                                                                               TRINICK J.;
ing of titin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26926
                                                                                PFUHL M., MC
e C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle ultrastructure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ation update)
(CONNECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ζ
                                                                                us of human
    INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
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                       Z
                                                                                                    PASTORE A.;
                                                                                cardiac
                       MUSCLE
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alignment_block:
US-09-240-675-1_COPY_27_427 x Q10466
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                                                                                                                                                                                                                                                                                     Percent
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                        10969
                                                                                                                                                                       10922 ValAspValAspLysThrGluValSerLeuValTrpAsnLysProAspAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X64698; CAA45939.1;
EMBL; X83270; CAA58243.1;
EMBL; X64697; CAA45938.1;
EMBL; X90568; CAA62188.1;
EMBL; X64699; CAA6218.1;
EMBL; X64699; CAA45940.1;
HSSP; P56276; ITLK.
PFAM; PF00047; 1g; 59.
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MOD_RES
MOD_RES
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                206
                                                                                                                                                162
                                                                                                                                                                                               112 GTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>+</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscle protein; Cytoskeleton; Structural protein; Calmodulin-binding;
Serine/threonine-protein kinase; Alternative splicing; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00726; LEXASERPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00069; pkinase; 1. PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
-!- SIMILARITY: TO THE CATALYTIC DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE
PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE
DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN AND ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
                                                                                   GGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTACTACT
|| ::::::||||||:::
                                                                                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112 IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
GCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACT
                     GluCysValValThrGlyLeuGln......GlnGlyLysThrTy 10981
                                                                                                                        gAspGlyGlySerProIleThrGlyTyrLeuValGluTyrGlnGluGluG
                                                                                                                                                GTCTGTCGGGAAT.....GTGACTTTTCATTCGATTATCAAAAAAACTG
                                               AAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATT
                                                                      lyThrGlnAspTrpIleLysPhe....LysThrValThrAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASES
                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                               Ratio:
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26178
26184
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22277
222449
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1372
1377
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1387
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                                                                                                                                                                                                                                                                                  80.00
1.379
58.586
                                                                                                                                                                                                                                                                                                                                                                                                                      4614
25070
25056
1372
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1382
1387
26171
26178
                                                                                                                                                                                                                       from: 1 to: 26926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....
                                                                                                                                                                                                                                                                                    Percent
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T -> P (IN REF. E -> G (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION PHOSPHORYLATION
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CATALYTIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALMODULIN-BINDING
                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                                                                                                                                                                                                Length:
Gaps:
Identity:
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                                                                                                                                                                                                                                                                                                                                                                                   REF.
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                                                                                                                                                                                                                                                                                                                                                            CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
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(BY PDPK)(POTENTIAL).
(BY PDPK)(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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4
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                                                                        10968
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10981 rArgPheArgValLysAlaGluAsnIleValGlyLeuGlyLeuProAspT 10998

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SARLE 
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US-09-240-675-1_COPY_27_427 x Q06349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_fung1:Q06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
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006349 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation updat
CHROMOSOME IV COSMID 9481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JIA Y., CHERRY J.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U28373; AAB64806.1; -.
SEQUENCE 442 AA; 50492 MW; 5073BCOA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATRELLLE P., LE T., MADIN S., MENEZES S.,
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
WILSON R., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DING
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STRAIN-S288C (AB972);
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C (AB972);
JOHNSTON M., ANDREWS S., BRINKMAN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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175 GTGACTTTTTCA..
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                                                                   yrSerAsn.....AspProAsnMetLysLys
                                                                                                                                         ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAAT 174
                                                                                                                                                                                                                                                                         AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                            ThrSerLeuIleValThrTyrMetGlyAlaGlyLeuLeuSerPheCys..
                                                                                                                                                                                                                                                                                                                                                                                                               ACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGC
                                                                                                                                                                                                      .....ArgAsnValLysLysAspSerGlnMetSerLysGluGlyIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: Q06349
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1.162
58.120
       .TTCGATTATCAAAAAACTGGGATGGATAATTGGAT
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 442
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seq_name: sp_invertebrate:045604
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                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                            WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSSY T., COOPER J., COULSON A.
CRANTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SOUNHAWMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                           Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z92811; CAB07274.1; -
EMBL; Z92789; CAB07274.1; JOINED.
EMBL; Z92789; CAB07223.1; JOINED.
EMBL; Z92781; CAB07223.1; JOINED.
EMBL; Z92811; CAB07223.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 045604; 045724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 A 366
                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1997)
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                               1083 AA;
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78.00
1.068
57.031
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                                                                                            1.
119604 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                               23EC3C85 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
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                                                                                                                                                                                                                                                                                                                                                           SHOWNKEEN R.,
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alignment\_block: US-09-240-675-1\_COPY\_27\_427 x 045604

Percent Similarity:

Percent

Identity: 24.219

Ratio:

Align seg

1/2

to: 045604

from: 1

to: 1083

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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_27_427 x Q65525
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                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: Q65525 from: 1 to:
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Q65525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JIANG B., GENTSCH J.R., TSUNEMITSU H., SAIF L.J., GLASS R.I.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U26551; AAB01672.1; -. PFAM; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
ROTAVIRUS C VP4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCT......TCATG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 spGlnValLysLeuLeuArgTrpAsnLeuLysAsnGluSerValPheAla 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
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Viruses; dsRNA viruses; Reoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
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                                                                                                                                                              63 GTCCGCAGCCGCA......GGTGGAAAAAAT.........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyArgTrpMetAlaSerGlyGlyGlySerGlyGlnIleLeuLeuTrpAs 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGGAT.....AATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....GGGAATGTGACTTTTTCATTCGATTATCAAAAAACTGG
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                                                                                                    uAlaAlaPheGluLeuTrpTyrGlyLysAlaAsnThrThrValThrSerA 126
                                                                                                                                                                                                                                                           SerThrValLysLeuLeuLysAsnGlyProGluSerTyrSerTrpAsnLe
                                                                                                                                                                                                                                                                                                                             ACGACCCTAGTGCTCGCCGTGGGCCCA.....rGGGTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Gaps: 8
Percent Identity: 23.810
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Last annotation update)
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                                      120
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alignment_block:
US-09-240-675-1_COPY_27_427 x Q08773
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                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                        seq_name: sp_fung1:Q08773
                                                                                                                                    Percent Similarity:
                                               Align seg 1/1 to: Q08773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         008773;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CHROMOSOME XV READING FRAME ORF YOR304W.
                                                                                                                                                                                                                                    Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z75212; CAAS9622.1; -. PFAM; PF00271; helicase_C; 1. PFAM; PF00176; SNF2_N; 1. SEQUENCE 1120 AA; 130326 MW; 51FC7F47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
CZIEPLUCH C., JAUNIAUX J.C., KORDES E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 uVal 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 AGTA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 rAsnLysValIleAsnPheSerTrpAsnValGlyGlyVal.....LeuI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
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                                                                                                                                                                                                                                                                                                                                                                                             TOBIASCH E.;
                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
GGTGGAAAAATCTA.....AAATCTCCCTCAAAAAGTAGAGGTCGACAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluMetLysMetValLysValLysArgGluGlySerIleAsnValAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spProTyrSerGlnIleArgAlaLeuGlnGlnProIleIleThrThrVal 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oArgSerAlaSerMetAsnIleTyrThrAspTyrTyrLeuAlaSerValA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...HighspSerLeuValLeuPheTrpAsnGluGlySerThrAlaLeuSe 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnPheThrSerAspSerPheAsnTrpGluGluTrpThrHisAsnPhePr 205
                                                                                                                                                                      Quality:
                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                    77.50
1.123
55.200
                                               from: 1 to: 1120
                                                                                                                                    Gaps:
Percent Identity:
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23.200
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664 GlyAlaLysAsnMetPheGluLysLysAlaSerLysValThrValAspAl

CATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCG

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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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Q20930 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 ATTTCGCAAAGCTCAGATTGGTCCT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        759 TyrLysGluIleIleGlyGlyGlySerLysSerAlaSerLysGlnThrPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       742 erArgArgGluArgArgArgGluGlnThrThrTyrSerValAspAspTyr 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 ..AGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 sSerPheGlnLysLysSerAsnAspLysValValGluTrpIleAsnProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 TTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 GlnLysPheAsnGlyIleGluAsnGlnSerAlaTyrGluTrpAsnGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 ATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 aAspIleAspAspIleLeuLysLysGlyGluGlnLysThrGlnGluLeu.
                                                                                                                                                                                                                    EMBL; 274037; CAA98493.1; -. PFAM; PF01421; Reprolysin; 1. SEQUENCE 508 AA; 57789 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 IleSerPheGlyAsnGluThrLeuHisMetValPheAlaGlyThrTrpIl
                                           350 TTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCA 393
                                                                                         222
                                                                                                                                    300 TAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGG 349
                                                                                                                                                                                                                           250 AGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAAT 299
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leAspLysPheThrIleTrpLeuLysGluGlnThrGlyLeuPro
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A_Geneseq_36:W21804
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A_Geneseq_36:W07702
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A_Geneseq_36:W82400
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A_Geneseq_36:W20115
A_Geneseq_36:W20540
A_Geneseq_36:R75075
A_Geneseq_36:W76186
A_Geneseq_36:W76186
A_Geneseq_36:Y04994
A_Geneseq_36:R32882
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Query: US-09-240-675-1_COPY_1_229
Query length: 229
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A_Geneseq_36:R14487
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A_Geneseq_36:W72048
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-MODEL-frame+_n2p.model -DEV-x1p
-O-/c9n2_1/USPTO_spool/US09240675/runat_30052000_164311_24603/app_query.fasta.1
-O-/c9n2_1/USPTO_spool/US09240675/runat_30052000_164311_24603/app_query.fasta.1
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-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
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-MAXIEN-1000000 -USER-US09240675 -NOPM-6 -ICPU=3 -NO_XLPXY -WAIT
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Ouaternary amine lipid compound
H. pylori secreted or periplasm
H. pylori secreted or periplasm
H. pylori secreted or periplasm
HCV core-envelope peptide NIN3N
Carbamoylphosphate-synthase hom
Actinoplanes sp. acarbose prote
Cancer suppressor transfer fact
Mycobacterium species protein s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out_format :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete interferon-alpha/beta Sequence of a soubble form of Human interferon receptor. Mond Human IFN receptor. Compsn. of Transmembranal interferon alpha
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A_Geneseq_36:R78519
A_Geneseq_36:P81936
A_Geneseq_36:W54097
A_Geneseq_36:R41227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: A_Geneseq_36:W21805
               PT New mammalian soluble interferon alpha-receptor forms - used for pri inhibiting, modulating or modifying the activities of interferon(s) PS Example 2; Fig 7; 46pp; English.

CC (Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (CC (W21805) is characterised by a new domain (S) which follows an CC (W21805) is characterised by a new domain (S) which follows an CC (W21805) is characterised by a new domain (S) which follows an CC (W21805) is characterised by a new domain (S) which follows an CC (W21805) is characterised by a new domain (S) which follows an CC (W21804). There is no transmembrane domain The amino acid compared to transmembranel CC sequence is predicted from a cDNA clone (see also T73520) obtd.

CC (Splice-deleted forms 1 and 2 (see also W21806) probably regulate CC the response of human cells to IFNs, either by acting as IFN CC antagonists or by regulating the activity of the multiple IFN CC modulate or modify the activities of IFNs alpha and beta in cells, this contains and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                            24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spliced-deleted interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W21805 standard; Protein; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interferon alpha-receptor;
                                                                                                                                                                                                                                                                               Ratovitski E, Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                       /label= Extracellular_domain
/label= Extracellular_domain
/note= "comprises amino acids 1-427 of the
transmembranal IFNAR"
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/label- S_
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1. .427
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117
108
107
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147
370
409
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alignment_scores:
Quality:
Ratio:
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US-09-240-675-1_COPY_1_229 x W21805
                                                                                                                                                                                                                                                                       Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                        Align seg 1/1 to: W21805 from: 1 to: 434
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                                                                                                                                                     AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                  CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC
                                                                                                    yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                           Percent Identity: 100.000
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seq\_name: A\_Geneseq\_36:R14487

227

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Pag Sed
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Quality:
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Percent Similarity:
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FR2557881-A.
09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
(EUB1-) LAB EURO BIOTECHNO.
EId P, Gresser I, Lutfalla G,
TOVEY MG, UZE G;
WPI; 91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New water soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; 52pp; French.

The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           documentation_block:
R14487 standard; Protein;
R14487;
R14487;
(first entry)
 R28495;
31-MAR-1993 (
Sequence of a
                                                 documentation_block:
                                     R28495 standard; Protein; 436
                                                                                                                        227
                                                                                                                                                                       177
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(first entry)
a soulble form
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: 5.075
: 100.000
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 (IFN) receptor
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PREDECTOR
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US-09-240-675-1_COPY_1_229 x R28495
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejections? Claim 2; Fig 1; S8pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (030533), was incubated with oligos 030534 and 030535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind of the IFN in the same way as antibodies on are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the contact of the transmender of known immunosuppressants such as steroids.
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
                                            Homo sapiens.
WO9507716-A.
                                                                                                                                                                                                                                                                                                                                                   Tovey M, Uze G;
WPI; 92-382110/46.
N-PSDB; Q30532.
                                                                         IFN receptor extracellular domain.
IFN receptor; interferon receptor; in
interferon-beta; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                          177
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17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
ELID P. Gresser I, Lutfalla G, Me
                                                                                                                                                                                                                                                              227
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Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                      L6-OCT-1995 (first entry)
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                                                                                                                                                     standard;
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E03114.
EP-402279
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: 5.075
: 100.000
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Gaps: 0
Identity: 100.000
                                                                                         interferon-alpha;
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                                                                            immunomodulator;
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    seq_name: A_Geneseq_36:W21806
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                                                                                                                                                                                                   AU9475977-A.
11-MAY-1995.
20-OCT-1994: 075977.
24-OCT-1993: IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
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WPI; 95-131187/1
N-PSDB; Q86457.
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W21806 standard; Pr
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23-SEP-1997 (first entry)
                 (ABRA) ABKAROYLUR (ABRA) ABKAR
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Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain
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inhibiting, modulating or modifying the Example 3; Fig 7; 46pp; English.
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Ratio:
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5.075
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/note- "comprises amino acid residues 1-413 and
422-427 of transmembranal IFNAR"
420. 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembranal IFNAR"
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/note= "comprises amino acids
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seq_documentation_block:
ID R11958 standard; Prot
AC R11958;
DT 18-JUL-1991 (first e
DE Human alpha IN; IFN
KW drug targetting.
OS Homo sapiens.
FY Key
FY Peptide 1...
PD 02-MAY-1991.
PF 19-OCT-1990; FF0-0758.
PR 20-OCT-1990; FF0-01377
PA (CNRS ) CNRS CENT NAT
PI MOGENSEN KE, UZE G, UZE G
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US-09-240-675-1_COPY_1_229
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Quality:
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Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                          20-OCT-1989; F00758.
(CNRS) CNRS CENT NAT RECH SCI. MOGENSEN KE, UZE G, Lutfalla G, Gr WPI; 91-148740/20.
N-PSDB; 011701.
New human
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      New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis disclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and discours of viral diseases and tumours. Antibodies raised against
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18-JUL-1991 (first entry)
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1. .27
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seq_name: A_Geneseq_36:R14488
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                                                                                                                                                                    09-AUG-1991.
05-FEB-1990; FR-001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
E1d P. Gresser I, Lutfalla G.
TOVEY MG, UZe G;
WPI, 91-319778/44.
N-PSDB; 014240.
New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematogus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful. Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Complete interferon-alpha/beta receptor.
IFN; autoimmune disease; graft rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
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Ratio:
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5.075
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Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID R28496
AC R28496
DE R28496
DE Sequence of a soulble
DE With a high affinity
Interferon receptor;
Synthetic.
PN W0921826-A.
PD 29-OCT-1992.
PN W0921826-A.
PD 17-APR-1991; F00318.
PF 17-APR-1991; W0-F0031
PR 17-APR-1991; W1-E91
PR W1: 92-382110/46.
DR W1: 92-382110/46.
DR W1: 92-382110/46.
DR W-PSDB; Q30533.
PT Water soluble polyper and beta - useful as placed in the same water for the IFN-alpha and -beta content of the IFN-alpha and -beta conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
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      N-PSDB; Q30333.

Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune of diseases and transplant rejection

Claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate

Claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate

claculation of the same way as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta really (203053), was incubated with oligos the IFN-alpha and -R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autolimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.

Sequence 557 AA;
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Ratio: 5.075
Percent Similarity: 100.000
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Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey M, Uze G;
WPI: 92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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alignment\_scores: Quality: Ratio:

340.00 5.075

Length: 67
Gaps: 0
Percent Identity: 100.000

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US-09-240-675-1_COPY_1_229
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US-09-240-675-1_COPY_1_229 x R42635
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                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
R42635 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis Disclosure; Fig 3; 21pp; English.

Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
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31-MAR-1992; 400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SA.
Benoit P, Maguire D, Meyer F, Plavec
WPI; 93-312951/40.
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/label- extracellular_domain
/note- "soluble, immunogenic
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seq_documentation_block:
ID R75356 standard; Prot
AC R75356;
DT 16-OCT-1995 (first e
DE Human IFN receptor: Interfe
KW IFN receptor: Locat
FH Key Incata
FT domain 1.4
PF 16-SEP-1994; E03114.
PF 16-SEP-1994; E03114.
PF 17-SEP-1994; E03114.
PF 17-SEP-1993; E0-40227
PA (EUBI-) LAB EURO BIOT
Compsn. of monoclonal
PT compsn. of monoclonal
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US-09-240-675-1
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Ratio: 5.075
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q86458.

Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.

The amino acid sequence of human interferon class I receptor is given in R73356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizzi EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFN receptor; interferon receptor; interferon-alpha; interferon-beta; monoclonal antibody; immunomodulato Homo saplens.
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AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
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                                                                                                                                                                                                                                                                                                                                                      to: R75356
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Percent Identity:
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alignment_block:
US-09-240-675-1_COPY_1_229 x W21804
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                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) bisclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
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                                          177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                         CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
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                                                                               lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                   AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
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437. .45
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458. .55
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5.075
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.557
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seq_documentation_block:

ID w93941 standard; Prot AC w93941;

AC w93941;

DT 30-JUN-1999 (first e DE Human brx protein; breast c anti-protein; breast c anti-cancer; anti-protein suppressor; ov KW immune tissue; prever os Homo sapiens.

PN w09915544-A1.

PD 01-APR-1999; U19782.

PR 23-SEP-1998; U19782.

PR 23-SEP-1998; U19782.

PR 23-SEP-1998; U19782.

PR (AUBI/) DRIGGERS P H.

PA (RUBI/) RUBINO D M.

(SEGE/) SEGERS J.

PI Driggers PH, Rubino I DR WPI; 99-254688/21.

DR WPI; 99-254688/21.

DR WPI; 99-254688/21.

DR Breast cancer gene en protein, brx

Claim lb; Page 58-62

CC This invention description has anti-cancer, ant transcription factor can be detected usin the kit) to determin cc ther proliferative diseas sequence 1429 AA;
seq_documentation_block:
ID W31867 standard; Protein; 1382
AC W31867;
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                                                                                                            seq_name: A_Geneseq_36:W31867
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                                                                                                                                                                        1282 uHis...ValArgArgGluAlaGlu......ArgLeuSerGln
                                                                                                                                                                                                                                                                                           1266 AspLeuGluArgLeuArgAlaAlaGlnLysGlnLeuGluArgGluGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                       1249 rpLysArgSerGlyArgSerSerSerArgArgArgAlaHisSerGlnTyr 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                           105 GGAAAAAATCTAAAAATCTCCCTCAAAAAAGTAGAGGTCGACATCATAGATGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1b; Page 58-62; 69pp; English.

This invention describes a novel human breast cancer gene encoding a nuclear receptor-binding auxiliary protein, brx. The brx encoded protein has anti-cancer, anti-proliferative and mitogenic activity and acts as a transcription factor and tumour suppressor. Levels of expression of Brx can be detected using the primers, probes and antibodies (contained in the kit) to determine a predisposition to breast and ovarian cancer and other proliferative disorders of immune tissues. Vectors containing the Brx gene can be used for prevention and treatment of cancers and proliferative diseases of mammalian reproductive and immune tissues.
                                                                                                                                                                                                                                 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                              155 CAACTT.....TATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RUBI/) RUBINO D M.
(SEGE/) SEGERS J.
Driggers PH, Rubino DM,
WPI; 99-254688/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1998; U19782.
23-SEP-1997; US-059621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer gene encoding a nuclear receptor-binding auxiliary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 CCCTAGTGCTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGA
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1.837
52.439
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Gaps: 6
Percent Identity: 41.463
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seq_documentation_block:

ID W07702 standard; Protein; 543

AC W07702;

DT 06-APR-1997 (first entry)

DE Mouse ETS2 repressor factor / 5
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US-09-240-675-1_COPY_1_229 x W31867
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                                                                                                                            seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse and human metastasis-associated p150-derived antigens - useful for raising antibodies for therapy and diagnosis of tumours Claim 3; Page 86-91; 111pp; English.

SC Claim 3; Page 86-92; 111pp; English.

This protein comprises a novel human 150 kDa cell surface metastasis-associated antigen, designated p150. It is the homologue of a novel murine p150 metastasis-associated antigen (see w31866). Its amino acid sequence was deduced from an isolated cDNA colone (see T93627). A claimed method for determining the metastatic potential of a tumour cell comprises assessing the level of p150 expression in the cell, a higher level of p150 expression in the cell, a higher level of p150 expression in the cell, a higher level of p150 expression in the cell, a higher interestion and consequently a higher metastatic potential. Immunogenic determinants of p150 and antibodies raised against them are useful in the diagnosis and treatment of metastatic potential in
                                                                                                                                                                    1035 AspArgGly 1037
                                                                                                                                                                                                                                                        1018 roArgArgGlyLeuAspGluAspArgGlySerTrpArgThrAlaAspGlu 103
                                                                                                                                                                                                                189 TCTGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                               985 spArgProSerTrpArgAsnThrAspAspAspArgProProArgArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               968 oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 952 ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr
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WPI; 97-549725/50.
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28-FEB-1997; GB-004161.
29-APR-1996; US-016487.
(NOVS ) NOVARTIS AG.
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Human metastasis-associated antigen p150.
Antigen; p150; metastasis; tumour; cancer; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 TCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCCGCAGG......
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                                                                                                                                                                                                                                                                                                TGAGG......TGGAACAGGAGCGATGAG
                                                                                                                                                                                                                                                                                                                                           AlaAspGluAspArgGlyAsnTrpArgHis.AlaAspAspAspArgProP 1018
                                                                                                                                                                                                                                                                                                                                                                                     TCCTCAAAAAGTAGAGGT.....CGACATCATAGATGACAACTTTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_36:W07702
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1.634
47.126
  factor (ERF)
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Gaps: 6
Percent Identity: 32.184
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seq_documentation_block:
ID R96994 standard; Prot
AC R96994;
DT 16-AUG-1996 (first e
DE Mouse IRS-2;
KW IRS-2; insulin recept
KW diagnosis; vector; an
OS Mus sp. Locat
FT domain 71abe
FT domain 71abe
FT domain 71abe
FT domain 71abe
FT modifled_site 74
FT modifled_site 74
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US-09-240-675-1_COPY_1_229/rev x W07702
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding ETS2 repressor factor - useful for reducing tumourigenicity, esp. oncogene associated tumour cells Disclosure; Page 70-72; 101pp; English.

Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS family and acts as a transcriptional repressor in mammalian cells. Its amino acid sequence was deduced from the murine ERF gene (T47198). Human ERF (see also W07700) has also been identified. ERF has tumour suppressor activity. Chimeric molecules comprising the ERF repressor domain in combination with a heterologous transcription factor having a binding domain can be used to reduce tumourigenicity associated with inappropriate expression of transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                               383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 TTCCACCTGCGGCTGCGGACAACACCCCATGGGCCCCACGGCGACGAGCACT
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Key
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05-JUN-1995; US-469412.
(USSH ) US DEPT HEALTH &
Athanasiou MA, Beal GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETS2 repressor factor; ERF; transcriptional repressor; tumour suppressor; tumour; cancer; oncoprotein; therapy.
                                                                                                                                                                                                                                                                                                            R96994 standard; Protein; 1321
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WPI; 97-0431
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                                                                                                                                                                                                                                         IRS-2; insulin receptor substrate-2; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                    58 AGGGTCGTCGCGCCCAGGAGGA.....CGACCATCATCTGGGAGC 19
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2.826
71.875
                                                                                   190. .366
/label= IH2
/note= "IRS-homology domain II"
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/note= "ets:like DNA binding
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       /note=
                                   /note= "IRS-homology domain III"
                                                                                                                                        /label= IH1
/note= "IRS-homology domain
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                                                        /label- IH3
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J, Blair DG, Fisher RJ,
   "common phosphorylation site"
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Gaps: 1
Percent Identity: 43.750
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/note-135. .:

.125 "unique f

phosphorylation

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alignment_scores:
Quality:
Ratio:
                                                                They insulin receptor substrate polypeptide and corresp. nucleic acid receptors, antibodies etc., useful for diagnosis, treatment and receptors, antibodies etc., also for diagnosis, treatment and receptor substrate. Also for drug screening bisclosure; Page 47-33; 105pp; English.

Mouse insulin receptor substrate-2, or IRS-2 (R96994), is a substrate for the insulin receptor, interleukin-4 receptor and can be phosphorylated by these receptors. It contains a number of phosphorylated by these common with IRS-1, showing the 2 proteins to be related. IRS-2 can be obtd. e.g. by affinity purification from insulin-stimulated FDC-P2 cells using immobilized SH2 domains of p85, or can be obtd. e.g. by affinity purification from insulin-stimulated sequence (T28933). Cells or animals having the IRS-2 transgene can be used to study insulin-related disorders, e.g. type II can be used to study insulin-related disorders, e.g. type II can be used to study insulin-related disorders, e.g. type II can be used to study insulin-related disorders.
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03-CCT-1995; U13041.
03-CCT-1994; US-317310.
03-CCT-1994; US-317310.
(JOSL-) JOSLIN DIABETES CENT INC.
(USSH-) US DEPT HEALTH 6 HUMAN SERVICES.
PIETCE JH, Sun XJ, White MF;
WPI; 96-20935121.
N-PSDB; T28293.
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/note- "unique phosphorylation site"
1060. 1065
/note- "unique phosphorylation site"
/note- "unique phosphorylation site"
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alignment_block:
US-09-240-675-1_COPY_1_229/rev x R96994
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1095 ysArgLeuSerLeu 1099
                                                                 1078 aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL 1095
                                                                                                                                                                                                 1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr
                                                                                                                                 1062 ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 1078
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                               17 GCCGCAGATCCCTG 4
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Search information block:
query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: Issued_Patents_AA:*
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Database length: 14437401
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-Q-/cgn2_1/USPTO_spool/US09940675/runat_30052000_164312_24612/app_query.fasta.
-DB-Issued_Patents_AA _QFWT-fastaan -SUFFIX-modif_rai
-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-XOOPEXT-0.000 -QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-328-256-11
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/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US92-00331-3
                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                         Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/328,256
APPLICATION NUMBER: US/08/328,256
ETILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
ETILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ABRAMOVICH, Carolii APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                            27 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                           TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
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                                                                       CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, Application US/08328256 5643749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acids
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                                                                                                                                                                                   to: US-08-328-256-11 from: 1 to:
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419 Seventh Street, N.W., Suite 300
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Percent Identity: 100.000
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31.7
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-307-588-2
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                                                                                                                                                            Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                              Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
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                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)672-5399 : INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 436 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 17:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard REGISTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
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27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGTCGCCGTGGG
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                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: SAXE, Bernhard D. REGISTRATION NUMBER: 28,665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Foley & Lardner
3000 K Street, N.W., Suite 500
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TOVEY, Michael G
                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                              Gaps:
Percent Identity:
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: 100.000
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-328-256-12
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                                                                                                                           alignment_scores:
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                                                              Percent Similarity:
                                                                                                                                                                                                                                                                             TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-CCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
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ADDRESSEE: BROWDY AND NEIMARK
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                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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                                                                                                        Quality:
                                                                                                                                                                                                                                                                   amino acid
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100.000
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Percent Identity:
                                                                100.000
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-328-256-10
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          alignment_scores:
Quality:
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                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 415 CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                 NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/328,256 FILING DATE: 24-OCT-1994
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERPERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                           STRANDEDNESS: single
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                                                                                                         protein
            340.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2,
                                                                                 PRIOR APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: IS 3/101-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-CCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                  INFORMATION FOR
TELECOMNU...
TELEPHONE: (703) 816 TELEPAX: (703) 816 TELEPAX: (707) NIXN UR
TOTEX: 200797 NIXN UR
TOTEX: TOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 NO CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A
ZIP: 22201-471
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UZE, Gilles
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                                                                                                                                                                                                                                                                                                                    VUMBER: US/08/471,454
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges
                                                                                                                                                                                                                                                                   US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2
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Percent Similarity: 100.000
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NIXON & VANDERHYE P.C.
                                                                    PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                           CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR
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Percent Identity: 100.000
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LENGTH:

557 amino acids

amino acid

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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-471-454-2
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-466-974-2
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Ratio: 5.075
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08466974 Patent No. 5861258
               APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, ION
TITLE OF INVENTION: CDUA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
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                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                     ZIP: 22201-4714
                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO.
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                                                                                                                                                                                                                                                                                                       VIRGINIA
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1100 NORTH GLEBE ROAD
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MBER: FR 89/13770
20-OCT-1989
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                                                                                                                                                                       Version #1.25
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-466-974-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFA: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,200 REGISTRATION NUMBER: 960-7 REFERENCE/DOCKET NUMBER: 960-7 TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ATTACATION
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR THE TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                         APPLICANT: MOGENSEN, Knud E. APPLICANT: U2E, Gilles APPLICANT: LUTEALLA, Georges APPLICANT: GRESSER, Ion
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                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
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STRANDEDNESS: sir
                                                                                                                                                          CITY: ARLINGTON
                                                                                                                                                                               STREET:
                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                      ADDRESSEE:
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                                                                                           22201-4714
                                                                                                                                  VIRGINIA
                                                                                                                                                                                 1100 NORTH GLEBE ROAD
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linear
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5.075
  PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:

Patentin Release #1.0, Version #1.25

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; TOPOLOGY: 1. ; MOLECULE TYPE: US-08-471-453-2
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US-09-240-675-1_COPY_1_229 x US-08-471-453-2
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                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-307-588-4
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Percent Similarity:
                                                                                                                                                                    Patent No.
                                                                                                                                                                                 Sequence 4,
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TELEX: 200797 NIXN UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: BYRNE, THOMAS E.
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                                                                                                                                                                                                                                                                                                                227 A 227
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                             APPLICANT:
                                                       APPLICANT:
                                                                          APPLICANT:
                                                                                             APPLICANT:
                                                                                                                              APPLICANT:
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APPLICATION NUMBER: FR 89/13770
PTITING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 15-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                   Application US/08307588
                                      INVENTION:
                                                 BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
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5.075
100.000
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                     MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
 INTERFERON
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Percent Identity: 100.000
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seq_documentation_block:
                                                                           seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
                       Sequence
Sequence 3, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: E
FILING DATE: 30-MAR-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                     227 A 227
                                                                                                                                                                                                                               177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                     127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
                                                                                                                                                                                                                                                                34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                        17 yProTrpValLeuSerAlaAlaAlaGlyGlyLySAsnLeuLySSerProG
                                                                                                                  67 s 67
                                                                                                                                                                                        51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                               77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 05-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/307,588
05-DEC-1994
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31-MAR-1992
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Gaps: 0
Percent Identity: 100.000
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APPLICANT:

Aguet, Michel Bohni, Ruth

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

STREET:

ADDRESSEE:

ITLE OF INVENTION:

Hemmi, Silvio

Receptor Subunit Polypeptides

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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-240-675-1_COPY_1_229 x PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 5.25 Inch, 360
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-
SOFTWARE: PATIN (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/16
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                   208 TTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                            158 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 207
                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                      17 nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                             1 GluAsnLeuLysProProGluAsnIleAsp***TyrIleIleAspAspAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 860
LECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                              heSerAlaGluTyrArg 39
                                                                                                                                 INFORMATION:
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T: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                   , Application US/08469412A 5856125
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amino acid
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     INVENTION:
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                                                       Fisher, Robert J.
Beal Jr., Gregory J
                                                                                            Blair, Donald G.
                                       Athanasiou, Meropi A
                                                                                                          Mavrothalassitis, George
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3.613
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Dionyssios N.
The ERF Genetic Locus and
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Gaps: 0
Percent Identity: 48.718
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 Its Products
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-469-412A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                  Sequence 64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                      NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                APPLICANT: WHITE, MOTTIS F.
APPLICANT: SUN, XIAO JIAN
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
                                                                                                                                                                                                                                                                                                                                         383 aGlyGluLysAlaProGlyGlyThrAspLysSerSerGlyGlySer 398
                                                                                                                                                                                                                                                                                                                                                                                                                          367 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 TTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..543
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                  58 AGGGTCGTCGCGCCCAGGAGGA.....CGACCATCATCTGGGAGC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Garrett-Wackowski, EugreGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 05-JU
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                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                4, Application US/08317310A
5858701
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Boston
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                      28 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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2.826
71.875
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(first 8 amino acids from first exon not
included)"
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Gaps: 1
Percent Identity: 43.750
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alignment_block:
US-09-240-675-1_COPY_1_229/rev x US-08-317-310A-64
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                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-683-743-4
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                                                                                                                                                                                                                                           Sequence 4,
                                                                                                       GENERAL INFORMATION:
APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1045 oThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1078 aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL 1099
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1062 ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GGAGATTTTAGATTTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CACGGCGACGACCACGACGTCGTCGCGCCCAGGA.....
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                                                                                                                                                                                                                                                                                                                                                                                            GCCGCAGATCCCTG 4
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                                                                                                                                                                                                                         , Application US/08683743 5843697
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1.984
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Gaps: 2
Percent Identity: 29.167
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-323-170B-2
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                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_1_229 x US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                            Sequence 2, Application US/08323170B Patent No. 5733772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: I
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                     APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Tau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                            CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                     210 TCATTCGATTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                          53 ThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                                                                                                                                                             36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Jersey
                      Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                    Townsend and Townsend and Crew LLP Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                              ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.50
1.922
59.259
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                                                                                                         Target Antigen, Pfs230
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US-08-317-310A-64

TOPOLOGY:

linear

protein

ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDPTELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

JDP-022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MSSOFTWARE: ASCII text

PC-DOS/MS-DOS

COUNTRY:

Massachusetts

02109

SOFTWARE: ASCII text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/317,310A FILING DATE: 03-OCT-1994 CLASSIFICATION: 435

TELEFAX: (617)227-594:
INFORMATION FOR SEQ ID NO:

: (617)227-7400 (617)227-5941 OR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS: LENGTH: 1321 amino acids TYPE: amino acid

California

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alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-469-427A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-240-675-1_COPY_1_229 x US-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-03: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-503.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/08/323,170B
                                                            APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alitalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL
THE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Quine, Jonathan A.
REGISTATION NUMBER: p-41,261
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 GGAGCGATGAGTCTGTCGGGAAT...GTGACTTTTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3135 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          819 ysGluAsnLysSerLeuGlyAsnLeuValAsnAsnSerValValTyrAsn 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803 rCysPheGlu...GluMetIleProTyrAsnLysGluIleLysTrpAsnL 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               787 SerGlyAspIleGlyGlyIleLeuPheProLysAsnIleLysSerThrTh 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/010,409 FILING DATE: 29-JAN-1993 TATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 AAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 TCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCCTCA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                              \DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                           Lys 836
                                                                                                                                                                                                                                           INFORMATION:
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GY: linear
                                                                                                                                                                                                                                                                                   Application US/08469427A
2: Evenson, McKeown, Edwards & Lenahan
1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3135 amino acids
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62.745
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576-0300
2:
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                                                                                                                     VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 37.255
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alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-469-427A-7
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Quality:
                     seq_documentation_block:
                                                             seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-609-443B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-469-427A-7 from: 1 to: 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 628-884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-MAR-1
                                                                                                      149 sProProCys 152
                                                                                                                                              193 TCGGGAATGT 202
                                                                                                                                                                                     133 ProfysfysGluSerAlaValLysProAspSerProArgIleLeuCy 149
                                                                                                                                                                                                                                                                      116 erGlnLeuGlyGluMetSerLeuGluGluHisSerGlnCysGluCysArg 132
                                                                                                                                                                                                                                                                                                                114 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE: adult mouse heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: EVANS, JOSEPH D
REGISTRATION NUMBER: 26,269
REFERENCE, DOCKET NUMBER: 41:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: PL
                                                                                                                                                                                                                                                                                                                                                       99 tGlnValProGlyProMetGlyGlnIleLeuMetIleGlnTyrProSerS 116
                                                                                                                                                                                                                                                                                                                                                                                               64 TCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                        83 ProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMe 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CCAGATGATGGTCGT......CCTCCTGGGCGCGACGACCCTAGTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/O
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 amino acids
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lication US/08609443B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER: US 08/397,651
01-MAR-1995
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1.611
51.429
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Patent No.

INFORMATION:

ERIKSSON, Ulf OLOFSSON, Birgitta

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alignment_scores:
Ouality:
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US-09-240-675-1_COPY_1_229 x US-08-609-443B-7
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                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA CODING THEREFOR NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS: Evenson, McKeown, Edwards & STREET: 1200 G Street, N.W., Suite 700
                                      116 erGlnLeuGlyGluMetSerLeuGluGluHisSerGlnCysGluCysArg 132
                                                                                 114 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
164 CCTGAGGTGGAACAGGAG......101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGIC TYPE: PI
                                                                                                                       99 tGlnValProGlyProMetGlyGlnIleLeuMetIleGlnTyrProSerS 116
                                                                                                                                                                    64 TCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAT 113
                                                                                                                                                                                                               83 ProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMe 99
                                                                                                                                                                                                                                                       23 CCAGATGATGGTCGT......CCTCCTGGGCGCGACGACCCTAGTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1200 G ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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Gaps: 2
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149 sproproCys 152

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Search information block:
Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: PIR_63:*
Database sequences: 16808
Database length: 58629743
Search time (sec): 85.570000
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pir2:S13141
pir2:T0357
pir2:T0357
pir2:T08907
pir2:T08930
pir2:T08930
pir2:T08930
pir2:T13088
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pir2:T13088
pir2:T13088
pir2:T130841
pir2:T28411
pir2:T3255
pir2:A46391
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pir2:A46391
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                                                                         p1r2:D64969
p1r2:JX0140
p1r2:JX0563
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p1r2:I46480
p1r2:I46480
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-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.l
-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164312_2000
-DB-PIR_63 -QFMT-fastan -SUFFIX-modif.rpr -GAPOP-12.000
-GAPEXT-4.000 -MINARCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-TGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-110.000 -XGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-TRANS-human40.cdi -LIST-45 -NORM-ext -MINLEN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
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     software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E Len : 557 | 560 | 590 | 590 | 304 | 304 | 304 | 1106 | 11106 | 571 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NO_XLPXY -WAIT
| O-antigen transporter - Escheri | Cytochrome-c oxidase (EC 1.9.3. | phosphate acetyltransferase - I | c-mer tyrosine kinase receptor | calcium channel BI-2 - rabbit | calcium channel BI-2 - rabbit | hypothetical protein (transducin hypothetical protein APE0658 - hypothetical protein R07B5.3 - hypothetical P07B5.3 - hypothetical P07B5.3 - hypothetical P07B5.3 - hypothetical R07B5.3 - hypothetical P07B5.3 - hypothetical R07B5.3 - h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I nuclear pore complex protein n hypothetical protein Y105C5B.o. hypothetical 119.5K protein (W hypothetical 19.5K protein T15N24.90 major polyhedral calyx protein DNA-packaging protein - phage N comc-alpha protein - phage T4 PRJ64 protein - chicken probable membrane protein MTCC MHC class I histocompatibility phospholipase C (EC 3.1.4.3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon alpha/beta receptor interferon alpha receptor type interferon alpha/beta receptor receptor interferon alpha/beta receptor hypothetical protein (ribosomal hypothetical protein F23K16.40 trp3 protein - rat
                                                                                                                                                                                                                                                 phosphoenolpyruvate carboxylase hypothetical protein SC1A9.25c DNA-directed RNA polymerase all hypothetical protein F08D12.9 tractin - medicinal leech probable cytochrome P450 monoox hypothetical protein T25F10.2 hypothetical protein T25F10.2 hypothetical protein T25F10.2
                                                                                                                                                                                                                                                                                                                                                                                                                        inversin - mouse

pR564/SC35 protein - human

splicing factor SC35 - human

cytokine receptor family II, me

cytokine receptor family class

cytokine receptor family class

CLM3 protein - yeast (Saccharom

hypothetical protein Rv0312 - M
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US-09-240-675-1_COPY_1_229
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            seq_documentation_block:
interferon alpha recepto
                                                                                 seq_name: pir2:S27387
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Percent Similarity:
                                                                                                                                                                                    227
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               receptor type 1 precursor
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: 5.075
: 100.000
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interferon alpha/Deta receptor precursor - hum C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: 22-Jun-1990 #sequence_revision 22-Jun-C; Accession: A32694; S17112 R; Uze, G; Lutfalla, G; Gresser, I. Cell 60, 225-234, 1990 A; Title: Genetic transfer of a functional huma A; Reference number: A32694; MUID: 90124632 A; Accession: A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pir2:T31639
pir2:A38845
pir2:S14016
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Gene: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:12021,
A;Map position: 21q22.1-11q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotekin; transmembrane #status predicted <TRN1>
F;1-21/Domain: transmembrane #status predicted <TRN2>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;ResIdues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross-references: EMBL:X60459; NID:g32671
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, July 1991 A; Description: The structuree of the human int A; Reference number: S17112 A; A; Accession: S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-557 <UZED
A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1;
59
59
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                                             176
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interferon alpha/beta receptor - mouse (Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C; Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429 R; Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A; Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A; Reference number: A45283; MUID:922625522 A; Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A; Accession: A45283; MUID:922625522
A; Note: sequence extracted R; Lutfalla, G.; Uze, G. Gene 148, 343-346, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Residues: 1-421, 'V', 423-560 <LIM>
A:Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:1-24/Domain: signal sequence alpha receptor type 1 #status predicted <MAT>
                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <UZE>
                                               A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A;Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha A;Reference number: S33770; MUID:93305725
A;Accession: S33770
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
R;Mouchel-Vielh, E; Lutfalla, G; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
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A; Residues: 1-560 < MOU>
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63
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6
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3.800
84.615
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Percent Identity:
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2
69.231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: IFNAR
A:Introns: 177/3; 331/1
                                                                                                                                                                                                                                                                                                                                                                                                                              alignment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DN/
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 426-445 <RE6>
A; Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DN/
A; Residues: 397-424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: 148423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-
A; Reference number: I48423; MUID:95047447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A;Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 265-375 < RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 243-264 < RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type:
A; Residues: 127-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
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A; Residues: 118-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
                                                                              180
                                                                                                                                     34 snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                    17
                                        51
                                                                                                                                                                                                                   80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                    30 ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                1 MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                oTrpValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA
                                      H1sGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg
                                                                         AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA
pir2:S13141
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seq\_documentation\_block:
hypothetical protein (ribosomal RNA repeat region) -

Giardia lamblia

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R:Upcroft, J.A.; Healey, A.; Mitchell, R.; Boreham, P.F.L.; Upcroft, P. Nucleic Acids Res. 18, 7077-7081, 1990
A;Title: Antigen expression from the ribosomal DNA repeat unit of Giardia intestinalis. A;Reference number: S13141; MUID:91088287
A;Accession: S13141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
hypothetical protein F23K16.40 - Arabidopsis thallana
C:Species: Arabidopsis thallana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X52949
A;Note: the source is designated as Giardia
A;Note: the assignment of the coding region
C;Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: the source is designated as Giardia intestinalis
A;Note: readthrough of the terminator TAG is supposed to occur between residues 241-Ala
R;Healey, A; Mitchell, R; Upcroft, J.A.; Boreham, P.F.L.; Upcroft, P.
Nucleic Acids Res. 18, 4006, 1990
A;Title: Complete nucleotide sequence of the ribosomal RNA tandem repeat unit from Giard
A;Reference number: S10886; MUID:90326542
A;Accession: S10886
alignment_block:.
US-09-240-675-1_COPY_1_229 x T09357
                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.40
A;Experimental source: cultivar Columbia; BAC clone F23K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_1_229/rev x S13141
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A; Residues: 1-294 <UPC>
                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                     A; Map position: 4
A; Introns: 129/2; 243/2
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-304 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z16652
A; Accession: T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: p1r2:T09357
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A; Residues: 1-241 <HEA>
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                                                                                                                                                                                                                                                                                                           A; Gene: ATSP: F23K16.40
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Percent Similarity:
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Percent Similarity:
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;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 24-Nov-1999
;Accession: S13141; S10886
                                                                                                                                                                                                                                                                                                                                          Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 AGGAGGACGACCATCATCTGGGAGCCGCCGCAGATCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oGlyAsnArgGlyAlaGlyGlyProArgArgArgSer 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGACAACACCCATGGGCCCACGGCGACGAGCACTAGGGTCGTCGCGCCC 44
                                                                                                                                              Quality:
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has been rev
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A;Status: nucleic acid sequence not shown
A;Molecule type; mRNA
A;Residues: 1-828 <PRE>
A;Experimental source; brain
C;Comment: This protein participates in store-operated Ca2+ entry into cells.
C;Superfamily: TRPC3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I. Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A;Title: Expression and characterization of a trpl homolog from rat. A;Reference number: JC5807; MUID:98042538
A;Accession: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-240-675-1_COPY_1_229 x JC5807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Rattus norvegicus (Norway rat)
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                                        209 TTCATTCGATTATCAAAAA 227
                                                                                      388
                                                                                                                                                                        371 etLysPheValAlaAlaSerPheIleIlePheLeuGlyLeuLeuValPhe
                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                     338 LeuValValLeuValValAlaLeuAlaLeuProPheLeuAlaIleGlyTy 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 sAsnThrAlaSerLeuGlyValValSerSerLeuLysMetLysLys.Leu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 AspAsnGlyArgHisHisHisAspThrProSerArgHisAspLysHi 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                     80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCT.... 125
                                                                                                                                                                                                                                                                                                                                                                                            30 ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 GATGATGGTCGTCCTGGGCCGCGACGACCCTAGTGCTCGTCGCCGT..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1...IleAspTyrProLys 409
                                                                                                                          AACAGGAGCGATGAGTCTGTCGGG......AATGTGACTTT 208
                                                                                                                                                                                                                 ..CAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysThrArgArgLysValArgGluProArgPheCysPheLysThrLeuSe 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTA 116
                                                                                    AsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIleThrVa 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .GAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCG
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Ratio:
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6
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1.614
60.274
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Percent Identity:
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3
34.247
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submitted to the EMBL Data Library, September 1999
A;Reference number: 220208
A;Reference number: 220208
A;Recession: T26391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-194 <WIL>
A;Residues: 1-194 <WIL>
A;Cross·references: EMBL:AL110479; NID:e1542153; PIDN:CAB54363.1; CESP:Y105C5B.o
A;Experimental source: clone Y105C5B
C;GenetLcs:
A;Gene: CESP:Y105C5B.o
A;Introns: 13/1; 56/3; 155/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclear pore complex protein nup153 - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Accession: S42718; S37477 R;McMorrow, I.; Bastos, R.; Horton, H.; Burke, B. Blochim. Biophys. Acta 1217, 219-223, 1994 A;Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup A;Reference number: S42718; MUID:94154002 A;Accession: S42718
                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Y105C5B.o - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C:Accession: T26391 R:MCMUITAY, A.
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US-09-240-675-1_COPY_1_229/rev x S42718
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A;Residues: 1-1475 <MCM>
A;Cross-references: EMBL:225535; NED:g406224; PIDN:CAA80982.1; PID:g406225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: p1r2:T2639:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: S42718
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     Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1298 SerSerAlaGlySerSerPheValPheGlyThr.GlyProSerAlaProS 1314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTTCCACCTGCGGCTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGACGACCATCATCTGGGAGCCGCCGC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erAsnAsnThrThrThrSerGlyPheGlyPheGlyAlaThrThrSer 1297
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Ratio:
                             Ratio:
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1.683
53.247
  68.50
1.756
69.643
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  Percent Identity:
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                             Gaps:
56
2
32.143
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3
33.766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 119.5k protein (uvrA region) - Micrococcus luteus N;Alternate names: ORF 1 protein C;Species: Micrococcus luteus, Micrococcus lysodeikticus C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993 C;Accession: JQ0405
C;Accession: JQ0405
C;Shiota, S.; Nakayama, H.
R;Shiota, S.; Nakayama, H.
A;Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: ident A;Reference number: S04781; MUID:89364717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1106 <SHI>
A;Coss-references: EMBL:X15867
A;Note: all the codons between
A;Note: the gene encoding this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-240-675-1_COPY_1_229/rev x JQ0405
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US-09-240-675-1_COPY_1_229 x T26391
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  seq_name: pir2:T08930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: JQ0405 from: 1 to: 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                  154 TCATCTATGATGTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTCC 105
                                                                                                                                                                                                                                                                                                         104 ACCTGCGGCTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 TCACATTCCCGACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GAGTCTGTCGGGAATGTG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 AGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGAT 185
                                                     93
                                                                                                     34
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                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 SerProThrGlyGluThrProValSerCysPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 GluGlnValAlaAsnMet 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 isIleAsnLeuLeu.....AsnGlyIleArgGlnLysAsnAlaIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 lLeuSerValThrValLysArgAsnMetThrGluTyrGluGlnLysIleH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 GTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 GTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLeuLeuArgAlaIleLeuLeuIlePheIleSer...AlaProTrpVa
                                                                                                                                                                                                                                                                                                                                                               .....CysProProLeuCysTrpProArgAlaGlnGluLeuLeuH
                                                  gProArgAlaGlnProGluGlyArgGlyCysGln 104
                                                                                                   ACCATCATCTGGGAGCCGCCGCAGATCCCTGCAG 1
                                                                                                                                                      ProArgArgAlaLeuGlyArgAlaGlyProHisArgArgProGlyAr
                                                                                                                                                                                                                                                         isHisArgLeuLeuArgArgArgGlyProArgArgArgProArgLeuArg
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1.875
46.154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent
                                                                                                                                                                                                                                                                                                            .....CGGACAACACCCATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identity:
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the

translat:

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A;Molecule type: DNA
A;Residues: 1-252 <AYR>
A;Residues: 1-252 <AYR>
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66761.1; PID:g559200
R:Oellig, C.; Happ, B.; Mueller, T.; Doerfler; W.
J. Virol. 61, 3048-3057, 1987
A;Title: Overlapping sets of viral RNAs reflect the array of polypeptides in the
A;Reference number: A43679; MUID:87311863
A;Accession: C43679
                                                                                                                                                                                                                                                          R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus A;Reference number: A72850; MUID:94303173
A;Accession: D72866
                                                                                                                                                                                                                                                                                                                                                                                                                                major polyhedral calyx protein - Autographa californica nuclear polyhedrosis virus C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV A;Note: dsDNA virus
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US-09-240-675-1_COPY_1_229 x T08930
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A; Residues: 1-571 <BEV>
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A; Accession: T08930
                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: D72866; C43679
                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 24-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: ATSP:T15N24.90
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A;Experimental source: cultivar Columbia; BAC clone T15N24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the Protein
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                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:D72866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pGlyTyr.....ArgTrpArgLysTyrGlyGlnLysValValArgGlyA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         luProArgValValValGlnThrLeuSer.GluValAspIleLeuAspAs 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTC.....GGGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gArgMetGluGlyAlaMetGluIleThrProLeuValLysProIleArgG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sn 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGCCCATGGGT.......GTTGTCCGCAGCCGCAGGT 104
  preliminary
e type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76/3; 90/3; 142/3; 311/1; 363/2; 415/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.00
1.711
55.882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 68
Gaps: 5
Percent Identity: 33.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
6
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C;Genetics:
A;Gene: Ac-PE/pp34
                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-252 <OEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status:
                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            packaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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    ω
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene 2
.CGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGC
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alignment_block:
US-09-240-675-1_COPY_1_229 x T13088
                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: phage lambda DNA packaging protein
C;Keywords: DNA packaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999 C;Accession: T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_1_229/rev x D72866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF064539; NID:g3192683; PID:g3192685; PIDN:AAC19038.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z17603
A; Accession: T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, submitted to the EMBL Data Library, May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: phage N15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: terminase large chain gp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-640 < HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: D72866 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                            Percent Similarity:
                                     101 GluLeuLeuTrpLeuProThrAspGlyAspAlaAspAsnPheMetLysSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 rArgSerProHis......CysArgPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 CTGTTCCACCTCAGGATAAAGTTGTCATCTATGATGTCGACCTCTACTTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TTTTTTGATAATCGAATGAAAAAGTCACATTCCCGACAGACTCATCGCTC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 PheTyrArgArgArgSerArgSerArgSerArgSerArgSerArgSe 112
                                                                                  8 GATCTGCGGCGGCTCCCAGATGATGGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rSerProArgArgGlyArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTGGGAGCCGCCGCAGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgProArgSerArgSerArgSerArgSerArgSerArgSerArgSerSe 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCATC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGAGGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                 Quality:
Ratio:
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                                                                                                                               to: T13088
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                                                                                                                                                                                                                                         63.00
1.340
47.475
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1.924
45.205
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Percent Identity:
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                                                                                                                               640
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4
26.263
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2
31.507
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77
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trans-

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comC-alpha protein - phage T4
N;Alternate names: gp comC alpha
C;Species: phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C;Accession: A45731
seq_documentation_block:
    PR264 protein - chicken
    C;Species: Gallus gallus (chicken)
    C;Date: 26-May-1994 #sequence_revision
    C;Accession: B42701; S17327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Title: Sequence and characterization of A:Reference number: A45731; MUID:93015705 A:Accession: A45731
A:Status: preliminary A:Molecule type: DNA A:Residues: 1-141 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: comC alpha
A;Map position: 5.848-6.274
C;Superfamily: phage T4 comC-alpha protein
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
                                                                                                                            seq_name: pir2:B42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                    42 CTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTC
                                                                                                                                                                                                                                                                                                 92 CGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGAT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yrArgGluLysSerValAspValValGlyTyrAspGluLeuAlaAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eThrAsnGlyArgGlyPheTrpCysLeuGlyGlyLysAlaAlaLysAsnT 167
                                                                                                                                                                                                                                                         sArgCysAlaGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspAlaAspIleGluLysGluGlySerProThrPheLeuGlyAsp 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GCCGCAGGTGGAAAAATCTAAAATCTC 123
                                                                                                                                                                                                                                                                                                                                         LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:M89919; NID:g215829;
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2.155
58.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                              to: 141
                        26-May-1994 #text_change 24-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the bacteriophage T4 comCalpha gene product,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:AAA32485.1; PID:g215832
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: 34.000
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A;Title: A potential splicing factor is encoded by the opposite strand of the A;Reference number: A42701; MUID:92212859
A;Accession: B42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                                                  C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-221 <VEL>
                                                                                                                                                                                                                                                                                                                                           A; Gene: MTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133
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seq_documentation_block:
probable membrane protein MTCC - Leishmania major
C; Species: Leishmania maior
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US-09-240-675-1_COPY_1_229 x B42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1998 A;Description: The nucleotide sequence of Leishmania major Friedlin chromosome A;Reference number: Z14740 A;Accession: T02841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Accession: T02841
R:Myler, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X62446; NID:g63751; PIDN:CAA44306.1; C;Superfamily: unassigned ribonucleoprotein repeat-containing F;15-82/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                    alignment_block:
US-09-240-675-1_COPY_1_229 x T02841
                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                     C; Superfamily: Saccharomyces probable membrane protein YOR271c
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-326 <MYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:T02841
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AE001274; NID:g3264850; PID:g1617564
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Percent Similarity:
                                                                 Align seg 1/1 to: T02841 from: 1
                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 lyArgArgSerArgSerProArgArgArgArgArgSerArgSerArgSer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 .... GGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 sHisSerArgArgGlyProProProArgArgTyrGlySerSerGlyTyrG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AGGGATCTGCGG....CGGCTCCCAGATGATGGTCGTCCTCCT.....
TGCGGCGGCTCCCAGATGATGGTCGTCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgSerArgSerArg
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	206	138	189	94	172	47	156
ri.	206 SerSerGlyGlnGlyIleArgValValAspAspAspGlyValThrArg 221		189 erCysAlaAlaThrValAsnLeuAlaSerMetArgLysAsnGluTrpLeu 205	94 CAGCCGCAGGTGGAAAAATCTAAAATCTCCCTCAAAAAAGTAGAG 137	172 yThrThrThrSerThrLeuIleArgAlaThrValProPheLeuAlaValS 189	47 CGCGACGACCCTAGTGCTCCCCCCCCGTGGGCCCCATGGGTGTTGTCCG 93	156 CysGlyGlySerLeuLeuAlaThrMetTrpLeuLysArgIleProThrGl 172

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Score_list:
Sequence
Swissprot_38:INR1_BUMAN +
Swissprot_38:INR1_BUVIN +
Swissprot_38:INR1_BUVIN +
Swissprot_38:INR1_MUMAN -
Swissprot_38:INR1_MUMAN -
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Database sequences: 83857
Database length: 30454973
Search time (sec): 45.030000
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Ouery: US-09-240-675-1_COPY_1_229
Ouery length: 229
Database: SwissProt_38.*
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-Q=/cgg2_1/USPTO_spoo1/US09246675/runat_30052000_164313_24686/app_query.fasta.1
-DB-Sw1ssProt_38 -QFMT-fastan -SUFFIX-mod1f.rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPOXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pCt
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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in ! Documentation ...

557 | P17181 homo sapiens (human).

560 | Q04790 bos taurus (bovine).

560 | Q2589 ovis aries (sheep). i

560 | Q2589 ovis aries (sheep). i

560 | Q2589 ovis aries (sheep). i

590 | P33896 mus musculus (mouse).

1475 | P49790 homo sapiens (human).

854 | Q34971 rathaylbacter rathayl

1382 | Q14152 homo sapiens (human).

551 | P70459 mus musculus (mouse).

141 | Q07506 homo sapiens (human).

552 | P24728 autographa californic

1321 | P31122 mus musculus (mouse).

141 | Q07438 bacteriophage t4. comc

221 | P33352 yallus yallus (chicke

730 | P06200 pseudomonas aeruginos

221 | Q01130 homo sapiens (human).

325 | Q08334 homo sapiens (human).

326 | P3355 saccharomyces corevis

982 | P23854 anabaena sp. (strain

339 | P77404 streptomyces coelicol

415 | P37746 escherichia coli. put

615 | P3262 bacillus subtilis. if

140 | P23452 bacillus subtilis. if

140 | P23452 bacillus subtilis. if

141 | Q08910 human papillomavirus

496 | P31260 homo sapiens (human)

441 | Q08910 human papillomavirus

496 | P31260 homo sapiens (human)

441 | Q08910 human papillomavirus

496 | P31260 homo sapiens (human)

441 | Q08910 human papillomavirus

496 | P31260 homo sapiens (human)

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496 | P31260 homo sapiens (human)

441 | Q08910 human papillomavirus

496 | P31250 homo sapiens (human)

441 | Q08910 human papillomavirus

60 | P30593 spiroplasma virus sp

178 | P1593 spiroplasma virus sp

189 | P2553 human papillomavirus

544 | P46936 gallus gallus (chicke

556 | P446 | P46936 gallus virus (strus)

556 | P3479 | pseudorabies virus

557 | P3479 | pseudorabies virus

558 | P16775 | P3479 |
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                                                                       | Q0138 bacteriophage t4. comc | P30352 gallus gallus (chick | P06200 pseudomonas aeruginos | Q0130 homo sapiens (human) | Q0130 homo sapiens (human) | Q01315 saccharomyces cerevis | P13365 saccharomyces cerevis | P23404 streptomyces coelicol | P37446 streptomyces coelicol | P3746 bacillus ps3 (thermop | P3745 bacillus ps3 (thermop | P3745 bacillus ps3 (thermop | P3745 bacillus ps5 | Q0110 human | P3150 homo sapiens (human) | Q80910 human papillomavirus t | P3150 homo sapiens (human) | Q80910 chlampdomonas reinhals | Q36372 plasmodium falciparu | Q36372 plasmodium falciparu | Q3736 methanococcus jannasc | P1964 lotus tetragonolobus | P1593 spiroplasma virus spv | P2553 brassica oleracea var | P20594 triticum aestivum (who | P2553 brassica oleracea var | P46936 gallus gallus (chicke | Q80903 mycobacterium tubercu | Q80903 myco
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SwissProt_38:SRFA_MOUSE
SwissProt_38:MMS3_MYCTU
SwissProt_38:TAP_DROME +
                               seq_name: SwissProt_38:INR1_HUMAN
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PIR; A32694; A32694.
PIR; S17112; S17112.
MIM; 107450; -.
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P17181;
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SUBCUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT CELLS.
EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
EYM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE INI-LIKE DOMAINS.
SIMILARITY: CHORAINS 2 FIBRONECTIN TYPE INI-LIKE DOMAINS.
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BY SIMILARITY.
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INTERFERON-ALPHA/BETA RECEPTOR ALPHA
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a collaboration

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SEQUENCE FROM N.A.

MEDLINE; 90124632.

Uze G., Lutfalla G., Gresser I.;

"Genetic transfer of a functional human interferon alpha receptor into mouse cells; cloning and expression of its cDNA.";
SEQUENCE FROM N.A.

MEDLINE; 92129376.

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;

The structure of the human interferon alpha/Deta receptor gene.";

J., Biol. Chem. 267:2802-2809(1992).
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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i Q60701 mus musculus (mo-
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US-09-240-675-1_COPY_1_229 x INR1_HUMAN
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Eutheria; Cetartiodactyla; Ru
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TISSUE-LUNG;
MEDLINE; 93076908.
MEDLINE; 93076908.
Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
"Specific antiviral activities of the human alpha interferons
determined at the level of receptor (IFNAR) structure.";
FEBS Lett. 313:255-259(1992).
[2]
                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last seq
01-NOV-1997 (Rel. 35, Last ann
INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                       SEQUENCE FROM
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RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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                                                                                                                                                a; Craniata; Vertebrata; Mammalia; Ruminantia; Pecora; Bovoldea; Bovi
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G -> A (IN REF. 2).
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alignment_block:
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MEDLINE; 93305725.

Lim J.-K., 93305725.

Lim J.-K., Langer J.A.;

"Cloning and characterization of a bovine alpha interferon receptor.";

Biochim. Biophys. Acta 1173:314-319(1993).

-i. FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
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CONFLICT
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SIGNAL
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PIR; S27387; S27387.
PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
             AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBURITS THEMSELVES.
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELULARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                               AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                            gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                             ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCCTCAAA
                                                                                                                                                                                              MetLeuAlaLeuGlyAlaThrThrLeuMetLeuValAla..
                                                                                                                                                                                                                              ATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                            snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln
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L06320; AAA02571.1;
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BY SIMILARITY.
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F -> V (EN REF. 2).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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seq_name: SwissProt_38:INR1_SHEEP
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 35, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
          CARBOHYD
CARBOHYD
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TRANSMEM
DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                    Receptor;
SIGNAL
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      SUBUNITS THEMSELVES.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE-ENDOMETRIUM;
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                                                                                                                                                                                        EMBL; X95939; CAA65183.1; -. EMBL; U65978; AAB84231.1; -. PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
"Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of an ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97135690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INTERFERON ALPHA/BETA RECEPTOR-1). IFNAR1 OR IFNAR.
                                                                                    CARBOHYD
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1109
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                                                                                                                                                                    Glycoprotein; Signal.
BY SIMILARITY.
                                                                                            EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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  EMBL; M89641; AAA37890.1;
PIR; A45283; A45283.
MGD; MGI:107658; IFNAR.
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alignment_block:
US-09-240-675-1_COPY_1_229
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SEQUENCE
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P33896;
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Eukaryota; Metazoa; C
Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib
                                                                                                      This
                                                                                                                                                                                                           Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
"Behavior of a cloned murine interferon alpha/beta receptor exp
in homospecific or heterospecific background";
in homospecific or interespecific background";
Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PRO
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BET
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send an email to license@isb-sib.ch).
                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: COUTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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US-09-240-675-1_COPY_1_229 x INR1_MOUSE
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N153_HUMAN STANDARD;
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SIGNAL
                   MCMOTROW I., Bastos R., Horton H., Burke B.;

"Sequence analysis of a CDNA encoding a human nuclear pore complex protein, hnup153.";

Blochim. Blophys. Acta 1217:219-223(1994).

-i- FUNCTION: POSSIBLE DNA-BINDING SUBUNIT OF THE NUCLEAR PORE COMPLEX (NPC). THE REPEAT-CONTAINING DOMAIN MAY BE INVOLVED IN ANCHORING COMPONENTS OF THE PORE COMPLEX TO THE PORE MEMBANE.

-i- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. LOCATED TO THE
                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153
                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 94154002.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTCGTCCTCGGGGGGGGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
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           TERMINAL RING STRUCTURE OF THE NUCLEOPLASMIC CAGE.
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REPEATS
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alignment_scores:
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ID KDPD_RATRA STANDARD;
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Bacteria; Firmicutes;
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Submitted (OCT-1997)
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                                   SEQUENCE FROM
                                                            Actinomycetales;
                                                                                                           i5-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
SENSOR PROTEIN KDPD (EC 2.7.3.-).
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                                                                                                                                                                                                                                                                  GAGGACGACCATCATCTGGGAGCCGCCGC
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utes; Actinobacteria; Actinobacteridae;
Micrococcineae; Microbacteriaceae; Rat
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alignment_block:
US-09-240-675-1_COPY_1_229 x KDPD_RATRA
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IF3A_HUMAN
STANDARD,
13-EBB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation FACTOR 3 SUBUNIT
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT
EUKARYOTIC TRANSLATION (EIF3 P185) (KIAA0139).
SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 96127530.
Nagase T., Seki N., 7
"Prediction of the co
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Eutheria; Primates;
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unidentified human
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J. Biol. Chem. 272:7106-7113(1997).
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Scholler J.K., Kanner S.B.;
"The human p167 gene encodes a unique structural protein that contains centrosomin A homology and associates with a multicomponent complex.";
DNA Cell Biol. 16:515-531(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D50929; BAA09488.1; -. EMBL; U58046; AAB41584.1; -. EMBL; U78311; AAB80695.1; -. MIM; 602039; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson K.R., Merrick W.C., Zoll W.L., Zhu Y.; "Identification of cDNA clones for the large subunit of eukaryotic translation initiation factor 3. Comparison of homologues from humourists."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initiation factor; Protein biosynthesis; Repeat; Phosphorylation.

25 x 10 AA TANDEM REPEAT OF D-[DE]-D-R-
[GP]-[PS]-[RW]-R-[GN]-[AM].

382 AA; 166568 MW; 485C01B28D67EBBA CRC64;
                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by lysis of cDNA clones from human cell line KG-1."; Res. 2:167-174(1995).
                             TGAGG.....
                                                                  AlaAspGluAspArgGlyAsnTrpArgHis.AlaAspAspAspArgProP
                                                                                                                                                                                                    oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 985
                                                                                                                                                                                                                                   TCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGG.......
                                                                                                                                                                                                                                                                   {\tt ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr}
                                                                                                                                                                                                                                                                                                    CCAGATGATGGTCGTCCT.....GGGCGCGACGACCCTAGTGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATED.
SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING METHIONYL-TRNAI AND MRNA.
{\tt roArgArgGlyLeuAspGluAspArgGlySerTrpArgThrAlaAspGlu}
                                                                                                  TCCTCAAAAAGTAGAGGT.....
                                                                                                                                   spargProSerTrpargasnThraspaspaspargProProargargIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST
                                                                                                                                                                  .....TGGAAAAATCT......AAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chem. 272:7106-7113(1997).
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                        67.00
1.634
47.126
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                   . CGACATCATAGATGACAACTTTATCC
                                   . TGGAACAGGAGCGATGAG
                                                                                                                                                                                                                                                                                                                                     to: 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                         32.184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIFFERENT
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Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                    1018
                                                                                                                                     1001
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seq\_name: SwissProt\_38:Y481\_HUMAN

STANDARD;

PRT;

483 AA

AspargGly 1037 TCTGTCGGG 197

189

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: Y481_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                          US-09-240-675-1_COPY_1_229/rev x Y481_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL PROTEIN KIAA0481 (HH1480).
KIAA0481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from human brain.";
DNA Res. 4:345-349(1997).
-1- SIMILARITY: SOME, TO HUMAN TEX28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
Nakajima D., Nomura N., Ohara O.;
"Characterization of cDNA clones in size-fractionated cDNA libraries
                                                                                                                                                                                                                                            172 CACCTCAGGATAAAGTTGTCAT...CTATGATGTCGACCTCTACTTTTTG
                                                                                                                                                                                                                                                                                                                       222 GATAATCGAATGAAAAAGTCACATTCCCGACAGACTCATCGCTCCTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein DOMAIN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB007950; BAA32326.1; -.
                                                                                                                                                                                                                                                                                       6
                                                                   84
                                                                                                                                        71
                                                                                                                                                                                                                56
                                 25
                                                                                                        75
rSerSerArgArg 104
                                   TGGGAGCCGCCGC 13
                                                                   LysArgGlyAlaSerLeuHisSerSerSerGlyGlyGlySerSerGlySe
                                                                                                       CCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCATCATC
                                                                                                                                      snArgValLeuGln.......GlnIleArgSerArgProSerIle
                                                                                                                                                                                                                rAlaMet.....SerLeuHisAspLeuProAlaArgProThrAlaPheA
                                                                                                                                                                                                                                                                                   AspSerProAspGluLysGluArgSerProGluMetHisArgValSerTy
                                                                                                                                                                          AGGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 34 F
483 AA; 52462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                65.50
1.598
57.746
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 71
Gaps: 3
Percent Identity: 33.803
                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLN.
A9EBB8EFD793D866 CRC64;
                                                                                                                                                                                                                                                                                                                                                          to: 483
                                                                                                                                                                                                                71
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                                                                                                                                                                                                                                                                                       56
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Seq_documentation_block:
ID ERF_MOUSE STANDARD;
AC P70459;
DT 15-JUL-1998 (Rel. 36, Creation of P70459;
DT 15-JUL-1998 (Rel. 38, Last DT 15-JUL-1999 (Rel. 38, Last DE ETS-DOMAIN TRANSCRIPTION FOR ENTER PROFILE FROM N.A.

OC Eutheria; Metazoa; Chorda OC Eutheria; Rodentia; Sciuro RP SEQUENCE FROM N.A.

RC STRAIM-129/SVJ;
RX MEDLINE; 97282708.

RA Liu D., Pavlopoulos E., MO "ERF; genomic organization or "ENF; genomic organization organization organization for the burden and the suis Instituce of the Suiss Instituce of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce of the European Bioinformatic organization of the Suiss Instituce organization organizati
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                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U58533; AAC09474.1; --
EMBL; U58534; AAC09474.1; JOINED.
HSSP. Q01543; IFLI.
MGD; MGI:109637; ERF.
MGD; MGI:109637; ERF.
PRONTS; PRO0454; ETS_DOMAIN.
PROSITE; PS00346; ETS_DOMAIN.1; 1.
PROSITE; PS00346; ETS_DOMAIN.2; 1.
PROSITE; PS00361; ETS_DOMAIN.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu D., Pavlopoulos E., Modi W., Moschonas N., Mavrothalassitis G.J.; "ERR: genomic organization, chromosomal localization and promoter analysis of the human and mouse genes."; Oncogene 14:1445-1451(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the companies of the ENTRY of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- PIM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
-!- PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Nurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1 ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED IN CELLULAR PROLIFERATION (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
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its

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regulation; Repressor; DNA-binding; Nuclear protein;
59050
¥.
                                               POLY-SER.
POLY-PRO.
                                                                           POLY-SER.
POLY-GLY.
SIMILARITY).
: 5AC1B72FB2743FE5 CRC64;
                               PHOSPHORYLATION (BY ERK2) (BY
                                                                                                             ETS-DOMAIN.
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alignment_block:
US-09-240-675-1_COPY_1_229/rev x ERF_MOUSE
                                                                                      alignment_scores:
Align seg 1/1
                                                      Percent Similarity:
                                                                  Quality:
Ratio:
to:
 ERF_MOUSE
                                                     65.00
2.826
71.875
from: 1 to: 551
                                                       Percent Identity:
                                                                            Length:
                                                       32
1
43.750
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375 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 108 TTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACT

391 59

58 AGGGTCGTCGCCCCAGGAGGA.....CGACCATCATCTGGGAGC 19

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alignment_scores
                                                                                                                                                                                                                                                                     alignment_block:
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                                                                                                                                                                                                               Align seg 1/1 to: VPHE_NPVAC
                                                                                                                                                                                                                                               US-09-240-675-1_COPY_1_229/rev x VPHE_NPVAC
                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vPHE_NPVAC STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
POLYHEDRAL ENVELOPE PROTEIN (PE) (POLYHEDRAL CALYX PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M17548; AAA66805.1; -. EMBL; L22858; AAA66761.1; -. PIR; C43679; C43679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus.";
Virology 202:586-605(1994).
-I- FUNCTION: MAJOR COMPONENT OF THE POLYHEDRA ENVELOPE.
-I- SIMILARITY: TO PE FROM OTHER BACULOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oellig C., Happ B., Mueller T., Doerfler W.;
"Overlapping sets of viral RNAs reflect the array of polypeptides
the EcoRI J and N fragments (map positions 81.2 to 85.0) of the
Autographa californica nuclear polyhedrosis virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Autographa californica nuclear polyhedrosis virus (ACMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391
                                     128
                                                                                                                                                                                                                                                                                                                                                                                                         Envelope protein; Viral occlusion body.

DOMAIN 98 140 ARG/SER-RI
SEQUENCE 252 AA; 29079 MW; 3252B0C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virol. 61:3048-3057(1987).
                                                                    rArgSerProHis
                                                                                         CTGTTCCACCTCAGGATAAAGTTGTCATCTATGATGTCGACCTCTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGlyGluLysAlaProGlyGlyThrAspLysSerSerGlyGlySer 406
                                   TTGAGGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATG
                                                                                                                                         PheTyrArgArgArgSerArgSerArgSerArgSerArgSerArgSe
                                                                                                                                                                            TTTTTTGATAATCGAATGAAAAGTCACATTCCCGACAGACTCATCGCTC
                                                                                                                                                                                                                                                                                                                                        Quality:
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                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                    63.50
1.924
45.205
                                                                                                                                                                                                                                                                                                   Length:
Gaps:
Percent Identity: 31.
                                                                                                                                                                                                               from: 1 to: 252
                                                                                                                                                                                                                                                                                                                                                                                                            ARG/SER-RICH.
3252B0C8E195A15D
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ArgSerArgSerProHisCys 126
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                                                                      CysArgPro
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                          DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                       MGD; MGI:109334; IRS2.
PRINTS; PR00628; INSULINRSI.
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                    Nature 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
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                                                                                     DOMAIN
                                                                                                       MOD_RES
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                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                         Phosphorylation.
                                                                                                                                                                                                                                                                                                                       HSSP; P35568; 1IRS
                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                             Glasheen E., Lane W.S., Pierce J.H., White M.F.; "Role of IRS-2 in insulin and cytokine signalling."; Nature 377:173-177(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95405472.
Sun X.J., Wang L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                             PFAM; PF00169; PH;
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                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: SKELETAL MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
                                                                                                                                                                                                                                                                                                                                                      HEART AND SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                   Wang L.-M., Zhang Y., Yenush L., Myers M.G. Jr. E., Lane W.S., Pierce J.H., White M.F.;
                                                                                                                            1242
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                                                     POLY-SER.
POLY-SER.
POLY-SER.
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                                                                                              PHOSPHORYLATION (BY SIMILARITY).
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(BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
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(BY SIMILARITY).
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                                           5069CE9D614960C7 CRC64;
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                                                                                                                                                   INSR)
                                                                                                                                                                                                                                                                                                                                                                 LIVER,
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alignment\_block: US-09-240-675-1\_COPY\_1\_229/rev x IRS2\_MOUSE

Percent Similarity:

Ratio:

63.50 1.984 44.444

Length: 72
Gaps: 2
Percent Identity: 29.167

Align seg 1/1

to: IRS2\_MOUSE

from: 1

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01-NOV-1991 (Rel. 20, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN)
EIF3S10 OR EIF3 OR CSMA.
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          JOSWIG G., Petzelt C., Werner D.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING METHIONYL-TRNAI AND MRNA.
-i- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fisher R., Fillmore H., Reynolds A.B.;
"Molecular cloning and characterization of the 162 kDa component of a multi-protein complex phosphorylated by Src.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petzelt C., Joswig G., Mincheva A., Lichter P., Stammer H., "The centrosomal protein centrosomin A and the nuclear protecentrosomin B derive from one gene by post-transcriptional protections of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IF3A_MOUSE
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 514-790 FROM N.A. (CENTROSOMIN A) MEDLINE; 91277032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       involving RNA editing.";
J. Cell Sci. 110:2573-2578(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  swig G., Petzelt C., Werner D.; urine cDNAs coding for the centrosomal antigen Cell Sci. 98:37-43(1991).
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seq_documentation_block:
ID COMA_BBT4 STANDA
AC 001438;
DT 01-OCT-1993 (Rel. 27,
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1995 (Rel. 31,
DT COMC-ALPHA PROTEIN.
GN COMCA OR GOF
OS Bacteriophage T4.
OC Viruses; dsDNA viruse
CC T4-like phages.
RN [1]
RP SEQUENCE FROM N.A.
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US-09-240-675-1_COPY_1_229 x IF3A_MOUSE
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Quality:
Ratio:
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EMBL; X84651; CAA59144.1;
EMBL; X17373; CAA35246.1;
                                         Bacteriophage T4.
Viruses; dsDNA viruses,
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MGD; MGI:95301; EIF3.
Initiation factor; Pr
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21 x 10 AA TANDEM REPEAT OF D-[DE]-1
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O -> H (IN REF. 2 AND 3).
A -> V (IN REF. 2 AND 3).
RHSR -> SIVA (IN REF. 3).
E -> D (IN REF. 2).
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[DE]-[PS]-[RW]-R-[GN]-[AM]-
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PRGKGAREGTNPSRTRANQEENCSGAVRADQEDR (IN
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alignment_block:
US-09-240-675-1_COPY_1_229 x COMA_BPT4
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
SFR2_CHICK STANDARD;
                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)
(SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Sequence and characterization of the bacteriophage T4 gene product, a possible transcription antitermination J. Bacteriol. 174:6539-6547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M89919; AAA32485.1; -. PIR; A45731; A45731.
                                                trans-spliced c-myb exon.;

Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).

FOR FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND INTERACTS WITH SPLICEOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND SPLICE SITES UDTRING SPLICEOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPS WITH PRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation.
SEQUENCE 141 AA; 16682 MW;
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 <del>: :</del>
                                                                                                                                                                      vellard M., Sureau A., Soret J., Martinerie C., Perbal B.;
*A potential splicing factor is encoded by the opposite st
                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTC
SUBCELLULAR LOCATION: ALTERNATIVE PRODUCTS:
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2.155
58.000
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Gaps: 3
Percent Identity: 34.000
 DIFFERENT FORMS
                NUCLEAR
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   PROTEIN MAY
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US-09-240-675-1_COPY_1_229 x
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                                                                                                                                                                                                                                                 _documentation_block:
                                                                                                                              PHIC_PSEAE STANDARD; PRT; 730 AA.

P06200;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
HEMOLYTIC PHOSPHOLIPASE C PRECORSOR (EC 3.1.4.3) (HEAT LAI
HEMOLYSIN) (PHOSPHATIDYLCHOLINE CHOLINEPHOSPHOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                  133
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PFAM; PF00076; rrm; 1.

Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
Phosphorylation.

16 21 RNA-BINDING (RNP2) (BY SIMILARITY).

DOMAIN 16 562 RNA-BINDING (RNP1) (BY SIMILARITY).

DOMAIN 111 116 GLY-RICH (HINGE REGION).

DOMAIN 117 221 ARG/SER-RICH (RS DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
MEDLINE; 86250607.
Pritchard A.E., Vasil M.L.;
                                                                                Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                               116 lyArgArgSerArgSerProArgArgArgArgArgSerArgSerArgSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                SEQUENCE FROM N
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PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES DOMAIN (BY SIMILARITY).

SIMILARITY: CONTRAINS 1 RNA RECOGNITION MOTIF (RNP).

SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING F
                                                                                                                                                                                                                                                                                                                                                                                                                TCCGC.....AGCCGCAGGTGGAAAAATCTAAAATCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGATCTGCGG...CGGCTCCCAGATGATGGTCGTCCTCCT......
                                                                                                                                                                                                                                                                                                              ArgSerArgSerArg 137
                                                                                                                                                                                                                                                                                                                                                 AAAAGTAGAGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                sHisSerArgArgGlyProProProArgArgTyrGlySerSerGlyTyrG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .... GGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTG
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B42701; B42701.
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116
221
25524
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2.083
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                                                                                  subdivision;
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Gaps:
Identity:
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L outstation -
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alignment_scores:
Quality:
Ratio:
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US-09-240-675-1_COPY_1_229 x PHLC_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: PHLC_PSEAE from: 1 to: 730
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Pritchard A.E.;

Pritchard A.E.;

Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: HYDROLYZES SPHINGOMYELLN IN ADDITION TO PHOSPHATIDYLCHOLINE.

-I- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = 1,2-DIACYLGLYCEROL + CHOLINE PHOSPHATE.

-I- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Bacteriol. 167:291-298(1986).
[2]
                                                                                                            443
                                                                                                                                                                    171
                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 39 730 HEMOLYTIC PHOSPHOLIPASE C. SEQUENCE 730 AA; 82655 MW; F1D3695824445FBF CRC64;
                                                       218
                                                                                                                                                                                                                     426 alLeuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
                                                                                                                                                                                                                                                                                163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M13047; AAA25966.1; -. PIR; A26391; A26391.
                                                                                                                                                                                                                                                                                                                                                                                         113 TCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTA 162
                                                                                                   ...TGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGA 217
|||:::|||:::||
ProTrpArgArgAla......ValCysGlyAspLeuThrSerLeuPheAs 457
                                                                                                                                                                                                                                                                       TCCTGAGG...... 170
pPheGln 459
                                                    TTATCAA 224
                                                                                                                                                                                                                                                                                                                                  .....LysValSerAlaGluValPheAspHisThrSerV 426
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1.824
49.275
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Gaps: 4
Percent Identity: 26.087
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Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database.
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sp_human:Q15778
sp_human:Q14152 +
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sp_phage:064317
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Database length: 69334122
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                                                                                                                                                                                                                              sp_invertebrate:002424 +
sp_invertebrate:Q23047 +
sp_rodent:Q60805 +
                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteria:086774
sp_bacteria:09X4V6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_bacter1a:Q9ZBS7
sp_human:Q9Y4L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_invertebrate:Q94603
sp_plant:023212
+
sp_mammal:077699 +
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                                                sp_invertebrate:Q21784
sp_fungi:Q9Y775 +
                                                                                                                                                                                   sp_human:Q9Y5L9
sp_virus:Q69088
                                                                                                                                                                                                                                                                                                         sp_plant:064410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_bacteria:007239
sp_bacteria:054272
                                                                                                                                sp_archea:Q9YEB6
                                                                                                                                                        sp_human:Q14396
                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:018465
                                                                                                                                                                                                                                                                                                                                                                 sp_rodent:Q9Z0H1
                                                                                                                                                                                                                                                                                                                                                                                       sp_invertebrate:P91232 +
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-Q-/cgn2_1/USPT0_spcol/US09240675/runat_30052000_164313_24664/app_query.fasta.1
-Q-/cgn2_1/USPT0_spcol/US09240675/runat_30052000_164313_24664/app_query.fasta.1
-DB-SPTREMBL_12 -QFMT-fastan -SUFIX-modif.rspt -GAPOP-12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELOPE-6.000 -DELEXT=7.000 -START1 - MARIX-blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-ALIGN=15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent:Q9WVR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:Q9W721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-1_COPY_1_229
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108 | Q9yeb6 aeropy....
184 | Q62143 mus musculus
021784 caenorhabd:
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358 !
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7 1077699 bos taurus (bovine). trp
0 1095927 homo sapiens (human). dj
62 1089019 mus musculus (mouse). i
62 108729 mycobacterium tuberculos
7 1054272 streptomyces hygroscopic
6 109w721 brachydanio rerio (zebra
4 109w725 brachydanio rerio (zebra
5 109w747 mus musculus (mouse). fx
9 109w747 mus musculus (mouse). fx
109w747 mus musculus (mouse). fx
109w747 mus musculus (mouse). fx
109w74 musculus (mouse). fx
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| 380 | O18465 hirudo medicinalis (m
| O64410 zea mays (maize). cytoch
| O2424 caenorhabditis elegans
| Q23047 caenorhabditis elegans
| Q60805 mus musculus (mouse). c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! Q15778 homo sapiens (human). ! Q14152 homo sapiens (human).
                                                                                                                                                      1 Q9y519 homo sapiens (human). t
1 Q69088 human herpesvirus 1. vi
Q14396 homo sapiens (human). liv
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064317 bacteriophage n15. termi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q30849 oryctolagus cuniculus
     Q21784 caenorhabditis el
Q9y775 candida tropicalis
P79321 sus scrofa (pig). k
088073 streptomyces coelic
                                                                                                                                Q9yeb6 aeropyrum pernix. 108aa
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Q60697 mus musculus (mouse). p
Q94603 leishmania major. mtcc
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sp_fung1:Q12405
sp_plant:Q08700
          SOC CON BRANCE SECTION SOC CON BRANCE DE LA CONTRACTOR DE
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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        Eukaryota;
Eutheria; |
                                                             Homo sapiens (Human)
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             Primates;
                                Metazoa;
                                                                                                             NUCLEAR
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Chordata; C Catarrhini;

Craniata; Vertebrata; i; Hominidae; Homo.

Mammalia

RECEPTOR-BINDING

Last sequence update)
Last annotation update)
TOR-BINDING AUXILIARY PROTEIN.

1429

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alignment_block:
US-09-240-675-1_COPY_1_229 x Q9YHW0
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                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                      REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082664; AAD13669.1; -:
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-MAY-1999 (TrEMBLrel. 10, Last annotation
INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                             6 CysAlaSerGlyArgLeuAlaAlaValLeuLeu...
                                            GCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAA 111
ATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTT
                                  lLeuValValValSer....
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Gaps:
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Q12405 saccharomyces cerev
Q08700 brassica napus (rap
Q9xfw6 brassica oleracea (
            161
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seq_documentation_block:
ID Q9XZV7;
AC Q9XZV7;
AC Q9XZV7;
DT Q1.NOV-1999 (TIEMBLEG DI O1.NOV-1999 (TIEMBLEG DI O1.NOV-1999) (TIEMBLEG DI O1.NOV-199) (TIEMBLEG DI O1.NOV-199) (TIEMBLEG DI O1.NOV-199) (TIEMBLEG DI O1.NOV-199) (TIEMBLEG DI O1.NO
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US-09-240-675-1_COPY_1_229 x Q9Y5T6
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1226 ArgGluLeuArg......AspGlyArgProSerTrp......
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DNA FOR RRNA TANDEM REPEAT UNIT (FRAGMENT).
Giardia lamblia (Giardia intestinalis).
                     MEDLINE; 91088287.
UPCROFT J.A., HEALEY A.,
"Antigen expression from
                                                                                                                                                                                                          HEALEY A., MITCHELL R., UPCROFT J.A., BOREHAM P.F.L., UPCROFT P., "Complete nucleotide sequence of the ribosomal RNA tandem repeat from Giardia intestinalis.";
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Submitted (FEB-1999) to the
EMBL; AF126008; AAD21311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RUBINO D., DRIGGERS P., ARBIT D., KEMP L., MILLER B., COSO O., PAGLIAI K., GRAY K., GUTKIND S., SEGARS J.; "Characterization of Brx, a novel Db1 family member that modulates estrogen receptor action."; oncogene 16:2513-2526(1998).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98288806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATGATAGATGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTAGTGCTCGTCGCCGTGGGCCCATGGGTTGTCCGCAGCCGCAGGT 104
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Ratio:
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                               MITCHELL R., BOREHAM P.F.L., the ribosomal DNA repeat unit
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EMBL/GenBank/DDBJ databases.
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seq_documentation_block:
ID 015778;
AC 015778;
AC 015778;
AC 01-NOV-1996 (TYEMBLTel. 01
DT 01-NOV-1998 (TYEMBLTel. 01
DT 01-NOV-1998 (TYEMBLTel. 02
DE 0167 (FRAGMENT).
OS HOMO SEPIENS (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90239007.
RA MEDLINE; 90239007.
RA MEDLINE; 90239007.
RA MEDLINE; SE, REYNOLDS A.B.
RT "MONOCIONAI Antibodies to
RT substrates of oncogene-ency
RL Proc. Natl. Acad. Sci. U.S
RN [2]
RP SEQUENCE FROM N.A.
RA SCHOLLER J.K., KARNER S.B.
RA SCHOLLER J.K.
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SEQUENCE FROM N.A.
MEDLINE; 90239007.
KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
"Monoclonal antibodies to individual tyrosine phosphorylated substrates of oncogene-encoded tyrosine kinases.";
substrates of oncogene-encoded tyrosine kinases.";
""" Natl. Acad. Sci. U.S.A. 87:3328-3332(1990).
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SEQUENCE FROM N.A.
SCHOLLER J.K., KANNER S.B.;
SCHOLLER J.K., KANNER S.B.;
SCHOLLER J.K., KANNER S.B.;
EMBL; U58047; AAB41586 1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; X52949; CAB44501.1; -.
NON_TER 286 286
SEQUENCE 286 AA; 28277 MW; 53B840
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                                                                   oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 69
                                                                                                                                                                                                ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr 52
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seq_documentation_block:
ID Q14152 PRELIMINA
AC Q14152; PO0653;
DT Q1-NOV-1996 (TrEMBLEE
DT Q1-NOV-1996)
OS HOMO Sapiens (Human).
OC Eukaryota; Metazoa; C
C Eukaryota; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa; Metazoa;
alignment_block:
US-09-240-675-1_COPY_1_229 x Q14152
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                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                     ZHU Y., JOHNSON K.R.;
Submitted (NOV-1996) to the P
EMBL; D50929; BAA094881; -.
EMBL; U58046; AAB41584.1; -.
EMBL; U78311; AAB80695.1; -.
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KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;

*Monoclonal antibodies to individual tyrosine-phosphorylated substrates of oncogene-encoded tyrosine kinases.";

Proc. Natl. Acad. Sci. U.S.A. 87:3328-3332(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOHNSON K.R., MERRICK W.C., ZOLL W.L., ZHU Y.; "Identification of cDNA clones for the large subunit of eukaryotic translation initiation factor 3. Comparison of homologues from humo Nicotiana tabacum, Caenorhabditis elegans, and Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96127530.

MEDLINE; 96127530.

MEDLINE; 96127530.

Prediction of the coding sequences of unidentified human recoding sequences of 20 per genes (KLARA0121-KLARA0160) danalysis of cDNA clones from human cell line KG-1."; DNA Res. 2:167-174(1995).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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PFAM; PF00019; TGF-beta;
PRINTS; PR00438; GFCYSKNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORITA K., CHOW K.L., UENO N.;
"Body Length and Male Tail Ray Pattern Formation of C. (
Regulated by a Member of TGFb Family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF074395; AAC26791.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CET-1
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GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGT
                                                nThrGlyAsnSerGluArgLysAsnArgLysLysGlyArgLysHisHis.
                                                                                                                GTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT
                                                                                                                                                                          GluProSerSerValArgArg.....LysArgSerArgGl
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A; 41781 MW;
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Last sequence update)
Last annotation update)
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Gaps:
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......AsnThrGluAlaGluSerAsnLeuCysArgArgThr 267

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SECTION OF THE PROPERTY OF THE
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US-09-240-675-1_COPY_1_229 x Q30849
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Quality:
seq_documentation_block:
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Percent Similarity:
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Q30849;
Q1-NOV-1996 (TREMBLrel. 01, Created)
Q1-NOV-1996 (TREMBLrel. 02, Last sequence update)
Q1-NOV-1999 (TREMBLREL. 12, Last annotation update)
MHC CLASS I ANTIGEN PRECURSOR;
ORYSTOLAGUS CUNICULUS (RABDIt),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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"Rabbit class I MHC genes: cDNA clones define full-length
of an expressed gene and a putative pseudogene.";
J. Immunol. 133:2261-2269(1984).
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                                                                                                                            lnThrGluArgAlaLysAsnThrAlaLeuSerPhe
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51.579
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358 MW;
39828 MW;
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MHC CLASS I ANTIGEN
; 86894130 CRC32;
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ID 064317 PRELIMINARY;
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US-09-240-675-1_COPY_1_229/rev x 088970
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01-NOV-1998
01-NOV-1998
01-NOV-1998
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"Partial genomic DNA sequence of mouse beta-cell IRS-2.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF090738; AAC61743.1;
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NON_TER
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SEQUENCE 734 AA; 75251 MW: B3410Car CECTO
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01-AUG-1998 (TrEMBLIEL.
01-AUG-1998 (TrEMBLIEL.
TERMINASE LARGE SUBUNIT.
                                                                                                                                                                                                                           HENDRIX R.W., RAVIN V.K., CASJENS S.R., FORD M.E., RAVIN SMIRNOV I.K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF064539; AAC19038.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 oThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 471
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSULIN RECEPTOR SUBSTRATE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GCCGCAGATCCCTG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 CACGGCGACGACCACTAGGGTCGTCGCGCCCAGGA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBLrel. 08, Created)
(TremBLrel. 08, Last sequence update)
(TremBLrel. 08, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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1.984
44.444
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                                                                                                                                                                                     73094 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                E1B34267 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734
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                                                                                                                                                                                                                                                                                                                                                                     FORD M.E., RAVIN
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2
29.167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
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63

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seq_documentation_block:
ID 013507 PRELIMINA
AC 013507, 000593;
DT 01-NOV-1996 (TIEMBLEE
DT 01-NOV-1996 (TIEMBLEE
DT 01-NOV-1999 (TIEMBLEE
DT 01-NOV-1999 (TIEMBLEE
DE TRANSIENT RECEPTOR PC
GN TRPC3 OR HTRP3.
OC EUKBRYOTA; Metazoa; C
C EUTHERIA; PRIMATES; C
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96234226.
RA ZHU X., JIANG M., PEY
RA BIRNBAUMER L.;
RA ZHU X., JIANG M., PEY
RA BIRNBAUMER L.;
RT capacitative Ca2+ ent
RT capacitative Ca2+ ent
RT CAPACITATIVE GA2+ CA1
RT CAPACITATIVE GA2+ CA1
RT CAPACITATIVE GA2+ CA1
RT COMBUCE FROM N.A.
RX MEDLINE; 97358541.
RA XU X.Z.S., LI H.S., C
RT COMBUCE TROM SEQUENCE FROM SEQUENCE FROM SEQUENCE FROM SEQUENCE FROM SEQUENCE FROM SEQUENCE FROM SEGUENCE FROM S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_1_229 x 064317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_human:Q13507
                                                                                                                                                                                                   alignment_scores:
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: 064317 from: 1 to: 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97358541.
XU X.Z.S., LI H.S., GUGGINO W.B., MONTELL C.;
"Coassembly of TRP and TRPL produces a distinct store-operated conductance";
conductance";
Cell 89:1155-1164(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN
TRPC3 OR HTRP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||
| 134 ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AACAGGAGCGATGAGTCTGTCGGGGAATGTGACTTTTTCATTCGAT 218
::: :: |||::: |||::: ||||||
                                                                                                                                                                                                                                                                                                                      EMBL; U47050; AAC51653.1; -.
EMBL; Y13758; CAA74083.1; -.
PFAM; PF00023; ank; 2.
PRINTS; PR01097; TRNSRECEPTRP.
SEQUENCE 848 AA; 97354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "trp, a novel mammalian gene family essential for agonist-activated capacitative Ca2+ entry.";
Cell 85:661-671(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 96234226.
ZHU X., JIANG M., PEYTON M.,
BIRNBAUMER L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 yrArgGluLysSerValAspValValGlyTyrAspGluLeuAlaAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 eThrAsnGlyArgGlyPheTrpCysLeuGlyGlyLysAlaAlaLysAsnT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 rHisValGluProThrIleArgAspValProSer.LeuLeuSerLeuAla 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GluLeuLeuTrpLeuProThrAspGlyAspAlaAspAsnPheMetLysSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATGG......GTGTTGTCCGCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCTGCGGCGGCTCCCAGATGATGGT..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....CGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GCCGCAGGTGGAAAAATCTAAAATCTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.340
47.475
                                                                        63.00
1.537
54.667
                                                       Length: 75
Gaps: 3
Percent Identity: 33.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 4
Percent Identity: 26.263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOULAY G., HURST R., STEFANI E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                               78AC2E9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID 060697;
AC 060697;
AC 07060697;
AC 07060697;
AC 07060697;
AC 07060697;
AC 07060697;
AC 07060697;
AC 070606998 (TTEMBLrel. 01)
AUG-1998 (TTEMBLrel. 07)
AUG-1998 (TTEMBLR)
AUG-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_1_229 x Q60697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: sp_rodent:Q60697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q60697 from: 1 to: 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-LYMPHOID TUMOR;
FISHER R., FILLMORE H., REYNOLDS A.B.;
SUBMITTED (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14172; AAA90910.1; -.
SEQUENCE 1344 AA; 161949 MW; 88593FEF CRC32;
986 ArgProSerTrpArgAsnAlaAspAspAspArgProProArgArgIleGl
                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                             969
                                                                                                                                                                                                                                                                                                                                                                                                                                                          952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        936 LeuArgArgLeuGlyGlyAspAspGluGluArgGluSerSerLeuArgPr
                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oAspAspAspArgIleProArgArgGlyLeuAspAspAspArgGlyProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGATGGTCGTCCTCCT.....GGGCGCGACGACCCTAGTGCTCGTC
                                                                                                                                                                                                                                                                                    rgArgGlyProAspGluAspArgPheSerArgArgGlyThrAspAspAsp 985
                                                                                                                                                                                                        .....TGGAAAAATCT......AAAATCTC
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1.432
42.718
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31.068

1002 123

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US-09-240-675-1_COPY_1_229 x Q13507
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                417 eThrValThr...AspTyrProLys 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 GACTTTTTCATTCGATTATCAAAAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 etLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeuLeu 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 rTrpIleAlaProCysSerArgLeuGlyLysIleLeuArgSerProPheM 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::|||||||::: ||| ||| :::::||| 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTGGAACAGGAGCGATGAGTCTGTCGGG......AATGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTAGAGGTC......GACATCATAGATGACAACTTTATCCTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: Q13507 from: 1 to: 848
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                  1344 AA
         Mus.
                                     Mammalia;
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seq_documentation_block:
ID. 023212 PRELIMI
AC 023212;
DT 01-JAN-1998 (TrEMBL
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US-09-240-675-1_COPY_1_229 x Q94603
                                                                  seq_name: sp_plant:023212
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Q94603 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SISK E., SUNKIN S., SWARTZELL S., WESTLAKE T., MAGNESS C., BASTIEN FU G., IVENS A., STUART K.;
"Leishmania major Friedlin chromosome 1 has only two polycistronic units of protein coding genes.";
Submitted (MAY-1998) to the EMBL/Gennant manual coding sets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002
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                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The nucleotide sequence of Leishmania major Friedlin chromosome Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB001274; AAC24664.1; -.
SEQUENCE 326 AA; 36141 MW; A629D498 CRC32;
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01-FEB-1997 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                               156 CysGlyGlySerLeuLeuAlaThrMetTrpLeuLysArgIleProThrGl 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida;
                                                                                                                                                                                 94
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                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                               CAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAG.....
                                                                                                                                                                                                                                                                                 yThrThrThrSerThrLeuIleArgAlaThrValProPheLeuAlaValS 189
                                                                                                                                                                                                                                      CGCGACGACCCTAGTGCTCGTC...GCCGTGGGCCCATGGGTGTTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCGGG 197
                                                                                                                                                    erCysAlaAlaThrValAsnLeuAlaSerMetArgLysAsnGluTrpLeu 205
                                                                                              SerSerGlyGlnGlyIleArgValValAspAspAspGlyValThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgArgGlyLeuAspAspGluArgGlySerTrpArgThrAlaAspGluAs 1035
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 (TrEMBLrel.
                             PRELIMINARY;
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1.645
57.576
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Last sequence update)
Last annotation update)
Created)
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                           PRT;
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seq_name: sp_mammal:077699
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ID 077699 PRELIMINARY;
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NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                WISSENBACH U., PHILIPP S., FLOCKERZI V;
"Cloning and analysis of TRP channels.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AJ006781; CAA07246.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrembLrel. 08, 01-NOV-1998 (TrembLrel. 08, 01-NOV-1998 (TrembLrel. 08, TRP3 PROTEIN (FRAGMENT).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TIEMBLIEL 10, I
01-NOV-1999 (TIEMBLIEL 12, I
SPLICING FACTOR-LIKE PROTEIN.
C7A10.670.
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HSSP; P19339; 2SXL.
PFAM; PF00076; rrm; 2.
SEQUENCE 573 AA; 63551
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                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1998) to the
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Ratio:
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1.645
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63551 MW;
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  WW.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  B9F9B808 CRC32;
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Gaps:
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                                                                                                                                                                                                                                                                                    Bovoidea; Bovidae;
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alignment_scores:
Quality:
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Percent Similarity:
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US-09-240-675-1_COPY_1_229 x 077699
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US-09-240-675-1_COPY_1_229 x 095927
                                                                                                                                                                                                                                                                                                                                                                                                       SORRAR RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID 095927 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 62.00
Ratio: 1.512
Percent Similarity: 54.667
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                                                                                                                                                                                           Align seg 1/1 to: 095927 from: 1 to: 290
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL031432; CAB37992.1; -. SEQUENCE 290 AA; 33613 MW; B59E0C18 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DJ465N24.2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
DJ465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
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44 rgSerHisSerArgValSerSerArgPheSerSerArgSerArgArgSer 60
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61 LysSerArgSerArgSerArgArgArgHisGlnArg 72

<sup>116</sup> AAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGA 151

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Title:
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Gapop 10.0 , Gapext 0.5
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1 GKNLKSPQKVEVDIIDDNFI..........WKIGVYSPVHCIKTTVENEL 203
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 1000000

Total number of hits satisfying chosen parameters:

188963

188963 seqs, 23686106 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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IIT 2 95 R28495 standard; Protein; 436 AA. R28495; 31-MAR-1993 (first entry)	181 LTSWKIGYYSPVHCIKTTVENEL 203	121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180 	61 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120 	1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60	Query Match 100.0%; Score 1072; DB 1; Length 436; Best Local Similarity 100.0%; Pred. No. 1.1e-101; Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps	(or deriv.) and an immunoglobulin such as : Q14240. 436 AA;	The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble	le polypeptide(s) with affinity for IFN-alpha treat e.g. lupus erythematosus, Behcet's dise a, diabetes mellitus, rheumatoid arthritis, ¢ 5, 52pp; French.	05-FEB-1990; 001298. 05-FEB-1990; FR-001298. 05-FEB-1990; FR-001298. (EUBI-) LAB EURO BIOTECHNO. Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE; TOVEY MG, UZe G; WPI; 91-319778/44. N-PSDB; 014239.	LT 1 87 87 87 87 87 88 87 814487 standard; Protein; 436 AA. R14487; 16-JAN-1992 (first entry) Soluble interferon-alpha/Deta receptor. IFN; autoimmune disease; graft rejection; histocompatibility. Homo sapiens. FR2657881-A. 09-AUG-1991.

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Claim 2; Fig 1; 58pp; English.
DNA encoding the water-soluble polypeptide with a high affinity for IFN alpha and beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN alpha and beta receptor (030533), was incubated with oligos 030534 and 030535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the
Compsn. of monoclonal antibodies against interferon useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig. 2A-2B; 105pp; English.
A recombinant soluble form of the human interferon c protein extracellular domain, given in R71723, was e
                                                                              16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI: 95-131187/17.
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R71723;
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IFN receptor extracellular domain.
IFN receptor; interferon receptor; interferon artibody;
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                                                       N-PSDB; Q86457.
Compsn. of monoclonal
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23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune
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17-APR-1991; WO-F00318.
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Eid P, Gresser I, Lutfalla G, Me
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                                                                                                                                               New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis
Disclosure; fig 4; 30pp; French.
This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residues 164 (Thr.) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
                                                                                                                                                                                                                                                                                           20-OCT-1989; FR-013770.
(CNRS ) CNRS CENT NAT RECH SCI.
Mogensen KE, Uze G, Lutfalla G,
                                                                                                                                                                                                                                                                       N-PSDB; Q11701
                                                                                                                                                                                                                                                                                   WPI; 91-148740/20.
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                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                             Human alpha-interferon receptor protein.
Human alpha IFN; IFN agonists; antiviral;
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19-OCT-1990;
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immunomodulatory monoclonal
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(EUBI-) LAB EURO BIOTECHNO.
EIG P, Gresser I, Lutfalla G
TOVEY MG, UZE G;
WPI; 91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
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Complete interferon-alpha/beta
IFN; autoimmune disease; graft
31-MAR-1993 (first entry) Sequence of a soubble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
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Mater soluble polypeptide(s) strongly bind interferon(s) alpha and beta useful as immunosuppressants, for treating auto:immune pr and beta useful as immunosuppressants, for treating auto:immune pr diseases and transplant rejection soluble polypeptide with a high affinity for Claim 3; Fig 2; 58pp; English.

CLAIM 3; Fig 2; 58pp; English.

CLAIM ancoding the water-soluble polypeptide with a high affinity for DNA encoding the water soluble polypeptide with a high affinity for CLAIM as template. For example, bacterlophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and beta receptor (Q30533), was incubated with oligos CLAIM and Q30535. R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind CLAIM in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the CAIM is side-effects of known immunosuppressants such as steroids.
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Best Local Similarity
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W0921826-A.

29-OCT-1992.

17-APR-1991; F00318.

17-APR-1991; W0-F00318.

(EUBI-) LAB EURO BIOTECHNOLOGIE.

Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE
Tovey M, Uze G;

WPI; 92-382110/46.

N-PSDB; 030533.
                                            EP-563487-A.
06-OCT-1993.
31-MAR-1992; 400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
BEOOIL P. Maguire D. Meyer F. 1
WPI; 93-312951/40.
                                                                                                                                                                                                                                            Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection;

cell proliferation; allograft rejection; systemic lupus erythematosus;

psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;

immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                          20-APR-1994 (first entry)
          Monoclonal antibody
                            P-PSDB; R42635
                                                                                                                                                                                                                                      Homo sapiens.
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/label= extracellular_domain
/note= "soluble, immunogenic"
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Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral infection.
                                                                                                                                                                                                                                                                                                                                                        Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.
The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EUBI-) LAB EURO BIOTECHNOLOGIE Benizri EJ, Tovey MG; WPI; 95-131187/17.
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23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
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interferon-beta; monoclonal antibody; immunomodulato
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Pred. No. 1.5e-101;
; Mismatches 0;
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Pred. No. 1.5e-101;
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20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                           IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21805) probably regulate the response of human cells to IFNA, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 2; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abramovich C, Ratovitski E, WPI; 95-200634/27.
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                                                              SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                              GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
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Pred. No. 3.
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3.5e-101;
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RESULT W21806

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 202; Conserv
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20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV C
(ABRA/) ABRAMOVICH C.
Abramovich C. Ratovitsk
WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mammalian soluble interferon alpha-receptor forms inhibiting, modulating or modifying the activities of Example 3; Fig 7; 46pp; English.
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W21806;
                                                                                         23-SEP-1997 (first entry)
Transmembranal interferon
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                                                                                                                                       W21804 standard;
W21804;
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                                                Homo sapiens.
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                                                                   Interferon alpha-receptor;
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                                                                                         alpha-receptor.
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Pred. No. 4.3e-101;
0; Mismatches 1;
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Best Local S
Matches 202
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20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV CO I
(ABRA/) ABRAMOVICH C.
                                                                               22-JAN-1998.
17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
KOTENKO SV, PESTKA S;
WPI; 98-110590/10.
N-PSDB; V19874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purposes.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21805) have been detected that lack this transmembrane membrane. Soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
rejection

Claim 2; Page -; 79pp; English.

This sequence is the human CRFB4 sequence, DNA encoding it is used in the recombinant DNA (I) of the invention. (I) comprises a sequence (S1) encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
                                                            New recombinant DNA and CRFB4 linked to
                                                                                                                                                                                                         CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease;
                                                                                                                                                                                                                       CRFB4 protein CRFB4; interl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abramovich C, Ra
WPI; 95-200634/27
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                               septic shock; immune
                                                                                                                                                                                                                                                                     W52296 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                  LTSWKIGVYSPVHCIKTTVENEL
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02; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557
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458. .59
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437. .45
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                                                             operator,
                                                                                                                                                                                                                                             entry)
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.557
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.457
                                                           comprises sequences encoding interleukin-10 perator, useful, e.g. preventing allograft
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Pred. No. 5e-101;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                                                                                                                       203
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                                                                                                                                                                                               organ rejection;
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Best Local Similarity 30.5
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for preventing organ rejection. A vector containing (I) is used to restore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit III-10 activity in cells. Antibodies specific for CRFB4 are used to measure and localise CRBF4, for diagnosis of defective II-10 activity. Fragments of (I) are used as primers or probes to assay CRBP4-specific RNA. Agonists/antagonists may be administered parenterally, orally or rectally especially by intravenous injection or directly into a tumour or
                                                                                                                                                                      15-JUN-1995.
07-DEC-1994;
09-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding CRFB4, both operably linked to expression control sequences. Cells containing (I) may be used to identify agonists/antagonist of IL-10. Agonists are potentially useful, e.g. for preventing allograft rejection, as vaccine adjuvants, for treatment of photosensitivity, inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, viruses, bacteria and parasites (especially intracellular pathogens) and
Novel interferon gamma receptor treatment of inflammatory bowel claim 3; Fig.2A; 86pp; English. The IFN-gamma receptor beta-subu
                                                                                 Aguet M, Boehni R
WPI; 95-224321/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allograft.
                                                                     N-PSDB; Q90808
                                                                                                   (HEMM/) HEMMIS.
Aguet M, Boehni R,
                                                                                                                                      (AGUE/) AGUET M.
(BOEH/) BOEHNI R
                                                                                                                                                                                                                        W09516036-A.
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                                                                                                                                                                                                                                                                                                                                                                                                           interferon-gamma-antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                           Interferon-gamma receptor beta subunit; muIFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                             IFN-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R75782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor beta-subunit.
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267. .332
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                                                                                                                                                                                                                                                                                                        /label- Extracelular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                     Hemmi
                                                                                                                                                                                                                                                                                           . 266
beta-subunit encoded by
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Pred. No. 4.1e-14;
9; Mismatches 86;
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                               beta chain
disease and
                                 ain polypeptide -
and liver damage
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                              PT Novel human 2cytor7 DNA encodes a type 2 cytokine receptor - useful profit treating renal, neural, pancreatic and prostatic diseases PS Claim 1; Pages 55-59; 72pp; English.

CC This represents the Zcytor7 cytokine receptor Zcytor7 is a ligand-complete of the complete of the type 2 cytokine complete of the cytopeptide and is a novel member of the type 2 cytokine complete of the cytopeptide and is a novel member of the Zcytor cytokine complete of the cytopeptide and intracciption promoter, a sequence complying a transmembrane and intracellular domain, or both, and a cytopeptide are combinant production of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is complete the cytor and cytor in the kidney, pancreas, prostate or nervous complete thation of cell in these organs. The antagonists and agonists can complete complete complete complete complete can be used to stimulate proliferation and complete complete can be used in the treatment of renal, neural, pancreatic and prostate complete complete can be used in the treatment of renal, neural, pancreatic and prostate complete can be used in the treatment of renal, neural, pancreatic and prostate complete can be used in the treatment of renal, neural, pancreatic and prostate can discount the can be used to stimulate proliferation and complete can be used to the can b
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Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2cytor7 cytokine receptor polypeptide.
Ccytor7; cytokine receptor; ligand-binding polypeptide; kidney; pa
type 2 cytokine receptor family; CRF2; prostate tissue; nervous ti
type 2 cytokine receptor family; CRF2; prostate tissue; nervous ti
agonist; cell proliferation; cell differentiation; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1998.
18-FEB-1998; U03029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
Sequence
                       diseases
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V57515
                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitmore TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 553
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No. 1.4e-12;
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Job time: 20019 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.4%; Score 144; DB 1; Length 337; Best Local Similarity 24.7%; Pred. No. 6.2e-07; Matches 56; Conservative 39; Mismatches 86; Indels
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22-AUG-1994; U09438.
20-AUG-1993; US-110119.
(UYNE-) UNIV NEW JERSEY.
Cook JR, Donnely RJ, Eme
Pestka S, Schwartz B, Sol
WFI; 95-106679/14.
N-PSDB; 084697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suppressing tumours in mammals with accessory factor 1 (AF-1) - for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1 DNA in gene therapy Disclosure; Fig 21A; 114pp; English.

The sequence is that of human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant cells.
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11-OCT 1995 (first entry)
Human IFN-gamma accessory factor-1.
Interferon-gamma; AF-1; tumour.
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WO9505847-A.
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||:|::
213 LYCVHVES 220
                                                                                                                                                                                                                              103 GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 PGTK------DSVMWALDGL6FTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                            160 RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVE 200
                                                                                                                                                         141 GPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR 193
194 SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMAD 240
                                                                                                                                                                                                                                                                                                           85 NCTQITATECDETAASPSAGEPMDENV----TIRLRAELGALHSAWVTMPWEQHYRNVTV 140
                                                                                                                                                                                                                                                                                                                                                                                           52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 LPAPOHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFKYTDSK-----WFTADIMSIGV 84
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                                                                                                                                                                                                                                                                                                                                                           LKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 AA;
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Maximum DB
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1 GKNLKSPQKVEVDIIDDNFI.........WKIGVYSPVHCIKTTVENEL 203
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Copyright (c) 1993 - 2000 Compugen Ltd
                                              /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/1aa/5COMB.pep:*
/cgn2_6/ptodata/1/1aa/FCTUS_COMB.pep:*
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123.039 Million cell updates/sec
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US-08-328-256-11
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US-08-471-454-2
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US-08-943-087-54
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Best Local Sim
Matches 203;
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Patent No. 5
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ZIP: 20004
 1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-328-256-11
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APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERI

TITLE OF INVENTION: PREPARATION AINUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                       TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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                     Similarity
                                                                                                                                                                                       434 amino acids
 Conservative
                   100.0%;
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Score 1072; DB 1;
Pred. No. 4.9e-112;
; Mismatches 0;
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                                                             Query Match
Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
TYPE: amino acid
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 92400902.0 FILING DATE: 31-MAR-1992 ATTORNEY/AGENT INFORMATION:
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                                                            Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/:
FILING DATE: 30-MAR-1993
 27
                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                         TOPOLOGY:
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GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
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                                                             Similarity
                                                                                                                                                                436 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                    (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGUIRE, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEYER, Francois
                                                                                                                                                                                                                  (202)672-5300
                                                                                                                                                                                                                                                                Bernhard D.
                                                                                                                            protein
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                                              Score 1072; DB 2;
Pred. No. 5e-112;
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; TOPOLOGY: 11
; MOLECULE TYPE:
US-08-328-256-12
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                                                                                                                                         Query Match
Best Local Sim
Matches 203;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/328.
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, EGWARD
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         TELLEFAX: 248633
               61 CNESSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BROWDY, Roger L.
REGISTRATION NUMBER: RE'
REFERENCE/DOCKET NUMBER:
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CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
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                                                                                                                                                            Similarity
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                     496 amino acids
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                                                                                                                                           Conservative
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                                                                                                                                         Score 1072; DB 1;
Pred. No. 6e-112;
; Mismatches 0;
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Patent No. 5643749
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                   Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BEOMITY DOCATION:
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LENGTH: 557 amino acids
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APPLICANT: RATOVITSKI, Edward
RITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
RITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202
TELEFAX: 248633
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
 181 LTSWKIGVYSPVHCIKTTVENEL 203
                                                                   121
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CITY: Washington
                                                                                                                                                                                                                                                    Local Similarity
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ZIP: 20004
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                                                                                                                                                                                    1-GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
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                                                                                                                  CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
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                                                   SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                  CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                                    GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
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                                                                                                                                                                                                                                  Score 1072; DB 1; Pred. No. 7.2e-112; Mismatches 0;
                                                                                                                                                                                                                                                                 Length 557;
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; MOLECULE TYPE:
US-08-471-454-2
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Patent No.
                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 816-410
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/900,64
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-CCT-1989
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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 181 LTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                     61 CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
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                                                                                                CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
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Pred. No. 7.2e-112;
Mismatches 0;
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Patent No.
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/1370
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
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LENGTH: 557 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TELEX: 200797 NIXN UR
TELEX: 200797 NIXN UR
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STRANDEDNESS: si
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LTSWKIGVYSPVHCIKTTVENEL 203
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                                                                                                                                                                      GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
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Pred. No. 7.2e-112;
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Matches 203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/900, FILING DATE: 15-JUN-1992 APPLICATION NUMBER: FR 89/137: FILING DATE: 20-OCT-1989 ATTORNEY/AGENT INFORMATION: NAME: BYRNE, THOMAS E. REGISTRATION NUMBER: 32,205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: NIXON & VANDERHYE P.C.
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TELECOMMUNICATION INFORMATION:
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APPLICANT: LUTFALLA, G
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TYPE: amino acid
STRANDEDNESS: single
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STATE: VIRGINIA
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LTSWKIGVYSPVHCIKTTVENEL 203
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US-08-307-588-4
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Best Local Similarity
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tent No. 5919453
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LENGTH: 557 amino acids
TYPE: amino acid
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FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ANTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
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MEDIUM TYPE: Floppy disk
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CITY: Washington
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                                                               SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
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3000 K Street, N.W., Suite 500
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PLAVEC, Ivan
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30-MAR-1993
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                                                                                                                                                                                                                                                                    Score 1072; DB 2;
Pred. No. 7.2e-112;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                    Length 557;
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Best Local S
Matches 98
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 8666
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Aguet, M
APPLICANT: Bohni, R
APPLICANT: Hemmi, S
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                    121
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181
                               181 LTSWKIGVYSPVHCIKTTVENE
                                                                                                                                                           62 NFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415/952-9881
                                                                                                                                      61 EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
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FILING DATE: 07-DEC-1994
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                                                                                                                                                                                                                                   2 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKC 61
                                                                                                   SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                           ENLKPPENIDXYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDERKWLKXPECQHTTTTKC 60
PSLKKHSNYSTXQCISTTVANK
                                                                  SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                                                                                                                                                                                               ch 45.8%;
l Similarity 48.5%;
98; Conservative 3
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South San Francisco
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Bohni, Ruth
Hemmi, Silvio
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Pred. No. 2.4e-47;
34; Mismatches 69
202
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US-08-683-743-4

Sequence 4, Application US/08683743 Patent No. 5843697 GENERAL INFORMATION:

GENERAL INFO APPLICANT:

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; Sequence 2, Application PC/TUS9414277
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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HYPOTHETICAL:
FRAGMENT TYPE:
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LENGTH: 325 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                   TITLE OF INVENTION: RENUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                         137
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                                                                                                                                                                                                                                                                                    182 TSWKIGVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                         67 KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                      DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                            -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
                                                                                                                                                                                                                                                                                                                                                         KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
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                                                                                      Bohni, Ruth
Hemmi, Silvio
                                                                                                                         Aguet, Michel
                                                                                                         Bohni,
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                    Genentech,
     Point San Bruno Blvd
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CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
CHAIN
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                                                                        Receptor Subunit Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 325;
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Matches 65
                                                                                                                                                                                                                                                                                                   Sequence 6,
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SEQUENCE CHARACTERISTICS
LENGTH: 332 amino acti
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                             NUMBER OF SEQUENCES: 8
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MEDIUM TYPE: 5.25 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
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                                                                                                                                                                                                                                                                                                                                                                                            198 KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
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                                                                                                       STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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TELEFAX: 415/-
TELEFAX: 910/371-7168
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                        COUNTRY:
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                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSXWVGLEPFQHYENVTVGPPKNIS
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65; Conserv
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 amino acids
                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                            Genentech,
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                                                                                                                                                                                                                Receptor Subunit Polypeptides
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pred. No. 2.4e-14;
pred. No. 2.4e-14;
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Indels 32;

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Best Local Similarity
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LENGTH: 223 amino acids
TYPE: amino acid
                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                      APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lok, S1
APPLICANT: Kho, Choon J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                           STREET: 1201 E
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                       PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 KPYRVYCLQTERQLILKNKKIRPHGLLSNVSCHETT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                        COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 NITSTKCNESS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LARPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/952-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                                                                                           COUNTRY: US
ZIP: 98102
                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARE: patin (Genentech)
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    5, Application US/08943087
5945511
                                                                                                                                                                                          1201 Eastlake Avenue East
                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                   Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415/952-9881
                                                                                                                                                                                                                                                                                                                 Jelmberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                          IBM Compatible
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                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.98;
                                                                                                                                                                                                                                                                                                                 Anna C.
                US/08/943,087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 192; DB 4; Pred. No. 8:1e-14; Pred. No. 8:3:
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; FRAGMENT TYPE:
US-08-943-087-56
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Best Local Sin
Matches 50;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                      STREET: 1- Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 TYCLKVKA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 LYCVHVES 191
                                                                                                                                        COUNTRY: U
ZIP: 98102
CLASSIFICATION:
                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                       USA
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 PGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 LSAETSDYEHQYYAKVKAIWGSKCSKWAESGRFYPFLESQIGPPEVALTSDEKSISVVLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                               INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08943087
                                                                                                                                                                                                                                                                                                                                              Jelmberg, Jelmberg, Jelmberg, Robyn /
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Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                          Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                  ZymoGenetics, Inc.
01 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.1%;
                                                                                                                                                                                                                                                                                                                                                                             Anna C.
                                                                                                                                                                                                                                                                                                                                      Theodore E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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PLICATION DATA:

AGENT INFORMATION:

20-FEB-1997

08/803,305

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; FRAGMENT TYPE:
US-08-943-087-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-943-087-50
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence 50,
                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ent No.
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REFERENCE/COCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          WERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 LYCVHVES 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 PGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                        STREET: 1201 F
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                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
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5945511
                                                                                                                                                                                                                                                                                                               T: Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                           WA
                                                                                                                                                                                                                                             E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                    Kho, Choon J
                                                                                                                                                                                                                                                                                                                                                                   Jelmberg, Anna C.
Adams, Robyn L.
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internal
                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 167.5; DB 2; Length y 26.1%; Pred. No. 4.5e-11; rvative 34; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                      Theodore E.
                                                   US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54:
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; FRAGMENT TYPE: internal
US-08-943-087-50
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Best Local Similarity 26.1%;
Matches 49; Conservative 3
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SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,743
REFERENCE/COCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
184 LYCVHVES 191
                                       171 TYCLKVKA 178
                                                                           128 APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT
                                                                                                                   122 PGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                                                                                                           68 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 127
                                                                                                                                                                                               63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/1
FILING DATE: 20-FEB-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                    8 LPKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 67
                                                                                                                                                                                                                                                                            4 LKSPOKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYOKTGMDNWIKLSGCONITSTKCN 62
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                                                                                                                                                                                                                                                                                                                                                          Length 221;
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Search completed: June Job time: 15448 sec ,1 2000, 04:17:54

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 1, 2000, 04:35:09 ; Search time 64.83 Seconds (without alignments)
. 183.585 Million cell updates/sec

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Title: Perfect score: Sequence: US-09-240-675-2\_COPY\_27\_229
1072
1 GKNLKSPQKVEVDIIDDNFI.....WKIGVYSPVHCIKTTVENEL 203

Total number of hits satisfying chosen parameters: 168808

168808 seqs, 58629743 residues

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR\_63:\*
1: pir1:
2: pir2:
3: pir3: pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

90	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	6	υ	4	w	2	1		Result
85. 5		87	87	7	87.5	88	89	89	89	89	10	89.5	90	90.5	92	N)		97.5	.7		111	144	199	214	216	219	525.5	708	1072		2010
в. О	80	•		8.2	•	•	•	•	•	٠	•	•	٠	8.4	8.6	•	8.9	9.1	9.1	9.1	10.4	13.4	•	20.0	•	•	49.0	66.0	100.0		Query
295	429	N	63	6805	~	515	1152	515	331	331	2215	2033	315	1304	477	292	925	7160	6839	6831	489	337	332	325	349	273	590	560	557		
۲	N	444	N	N	N	2	N	N	2	N	N	N	μ.	فسو	N	۲	N	N	N	N	N	N	N	N	N	N	N	N	N	: 6	
KFHU3	S59773	I38344	JC1391	S20901	A49667	139073	S20106	S59502	S59501	A54295	T00348	T09123	S14222	A46546	A34368	KFBO3	T29585	T27935	S57242	T27934	A31555	I38500	A49947	A47003	JC6311	G01418	A45283	S27387	A32694		3
tissue factor prec	26S proteasome reg	titin, cardiac mus	pe molec	titin - rabbit (fr	interleukin-10 rec	terferon al	hypothetical prote	interferon recepto		interferon alpha/b	LR11 protein - mou	hybrid receptor So	chalcone reductase	leukocyte common a	eron gan		-	ica		al prot	gamma	gamma	interferon gamma r	cytokine receptor	terfero	•	interferon alpha/b		interferon alpha/b		70000111111101

B

207 LTSWKIGVYSPVHCIKTTVENEL 229

interleukin-3 rece	A40091		878	7.5	80	(J
valosin-containing	S39110	-ب	780	7.5	80	4
frazzled gene prot	T13823	ຸ	1526	7.6	81	w
frazzled gene prot	T13822	N	1375	7.6	81	N
hypothetical prote	S67208	N	1120	7.6	81	-
hypothetical prot	C64483	N	1009	7.6	81	0
tissue factor prec	KFRB3	_	292	7.6	81.5	9
titin, muscle - c	A48721	N	817	7.6	82	œ
interleukin-5 rece	S12357	N	415	7.6	82	7
hypothetical prote	S01519	2	1068	7.7	82.5	თ
capsular polysacci	B64432	N	406	7.7	82.5	G
probable protein	A25698	N	306	7.8	83.5	4
probable membrane	S64916	N	1220	7.9	84.5	ω
glycoprotein E -	VGBE68	ᆫ	623	7.9	84.5	3
interleukin-10 rec	156215	Ŋ	578	8.0	85.5	۲

## ALIGNMENTS

	Qy 181 LISWKIGYYSPVHCIKTIVENEL 203	
PETTYCLKVKAAL 180               PETTYCLKVKAAL 206	Oy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 	
HLEAEDKAIVIHI 120              HLEAEDKAIVIHI 146	Qy 61 CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 	
VIKLSGCQNITSTK 60	OY 1 GKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK	
Length 557; Indels 0; Gaps 0;	Query Match 100.0%; Score 1072; DB 2; Lei Best Local Similarity 100.0%; Pred. No. 3e-87; Matches 203; Conservative 0; Mismatches 0; Inc	
e protein /Binding site: carbohydrat	C:Reywords: cytckine receptor; glycoprotein; transmembrane protein r;1-21/Domain: transmembrane #status predicted <trn1> F;437-455/Domain: transmembrane #status predicted <trn2> F;437-455/Domain: transmembrane #status predicted <trn2> F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding</trn2></trn2></trn1>	
381/3; 432/1; 480/3	A;Gene: GDB:IFNAR1; IFNAR; IFRC A;Gene: GDB:IFNAR1; IFRC A;Cross-references: GDB:120078; OMIM:107450 A;Map position: 21q22.1-21q22.1 A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1;	
alpha/beta receptor gene.	submitted to the EMBL Data Library, July 1991 A;Description: The structuree of the human interferon alpl A;Reference number: S17112	
PIDN:AAA52730.1; PID:g306914	NA UZE> GB:J03171; NID:g184645;	
on alpha receptor into mous	R;Uze, G.; Lutfalla, G.; Gresser, I.  Cell 60, 225-234, 1990  A;Title: Genetic transfer of a functional human interferon alpha A;Reference number: A32694; MUID:90124632  A:Accession: A33694	
#text_change 22-Oct-1999	ecursor - human ision 22-Jun-1990	

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Interferon alpha receptor type 1 precursor - bovine C:Species: Bos primigenius taurus (cattle) C:Jan-195 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C:Accession: S27387; S3770 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G. FEBS Lett. 313, 255-259, 1992 A:Title: Specific antiviral activities of the human alpha interferons are de A:Reference number: S27387; MUID:93076908
                                                                                                                                                                                                            interferon alpha/beta receptor - mouse
;Species: Mus musculus (house mouse)
;Species: Mus musculus (house mouse)
;Species: Mus musculus (house mouse)

C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429

R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.

Proc. Natl. Acad. Sci. U.S. A. 89, 474-44778, 192;

A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in A;Reference number: A45283; MUID:92262522

A;Atccession: A45283

A;Status: preliminary
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Biochim. Biophys. Acta 1173, 314-319, 1993
A:Title: Cloning and characterization of a bovine alpha
A:Reference number: S33770; MUID:93305725
A:Accession: S33770
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C:Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 *status predicted
Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta
A;Reference number: 148423; MUID:95047447
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A;Residues: 1-421,'V',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1;
                                                                                 A; Note: sequence extracted R; Lutfalla, G.; Uze, G.
                                                                                                       A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-590 <UZE>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPPGTKDSIMWAMDRSSFRYSVVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN
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137; Conserv
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Pred. No. 5.1e-55;
8; Mismatches 35;
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NCBIP: 102357)
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A; Accession: I48423
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 118-125 <
                                                                                                                                                                               RESULT
G01418
                                                                                               cytokine receptor family II, member 4 - human cyspecies: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision O6-Jun-C;Accession: G01418
submitted to the EMBL Data Library, R; Reference number: G06935 A; Accession: G01418 A; Status: preliminary; translated fi
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 265-375 <RE4>
                                                                                  R; Lutfalla, G.
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C; Keywords: cytokine receptor; transmembrane protein
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A; Residues: 473-590
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A; Residues: 426-445 < RE6>
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A; Residues: 397-424 < RE5>
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A; Residues: 127-224
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A; Residues: 243-264
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Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1;
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                                                                                                                                                                                                                                                                                     LLTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                              CNFSSLKLNYYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDEAKWLKVPECQHTTTTK 85
                                                                                                                                                                                                                                                            HPSLKKHSNYSTVQCISTTVANKM 229
                                                                                                                                                                                                                                                                                                                                          ISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAI 205
                                                                                                                                                                                                                                                                                                                                                                           ISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                       CEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVH 145
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104; Conserv
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Pred. No. 7.8e-39;
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                                                           April 199
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                                                                                                                       #text_change
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from

GB/EMBL/DDBJ

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interferon receptor-class II cytokine receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #te: C;Accession: JC6311 R;Gibbs, V.C.; Pennica, D. Gene 186, 97-101, 1997 A;Title: CRFZ-4:isolation of cDNA clones encoding the later of the later
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A; Accession: JC6311
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A;Cross-references: GDB:138168; OMIM:123889
A;Map posttion: 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                 RESULT
A47003
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A; Residues: 1-273 <LUT>
cytokine receptor family class
C; Species: Homo sapiens (man)
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A; Residues: 1-349 <GIB>
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Matches 60
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Best Local Similarity
Matches 58; Conserv
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nes 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH-ISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                                                QVQGFLLDQNRTGEWSEPICERT
                                                                                                                                                                                                                                                                                     KVKAALLTSWKIGVYSPVHCIKT 197
                                                                                                                                                                                                                                                                                                                                                                                                                  -----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRNKAGEWSEPVCEQTT 213
                                                                                                                                                                                                                                                                                                                                                       QIENEPET----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPWTTYCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLELRFSAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.1%; Score 216; DB 2; Length 349; ilarity 28.6%; Pred. No. 1e-11; Conservative 43; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 3.9e-12;
1; Mismatches 84;
                                                                                                                                                                                                                    212
                                    protein CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-Jul-1999 #text_change 16-Jul-1999
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                                        precursor -
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C;Date: 09-Sep-1994 #sequence_revision of the C;Accession: A47003
R;Lutfalla, G; Gardiner, K; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps A;Reference number: A47003; MUID:93300510
A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hemmi, S.; Bohni, R.; Stark, G.; Dr. Marce, T., Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-332 <HEM>
A;Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C;Keywords: cytokine receptor
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N;Alternate names: IFW-gamma R beta chain; IFW-gamma R species-s
C;Species: Mus musculius (bouse mouse)
C;Date: 06-Oct_1994 #sequence_revision 18-Nov-1994 #text_change
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C;Keywords: transmembrane protein
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A; Residues: 1-325 <LUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 TSWKIGVYSPVHCIKTT 198
                                                                                                          Match 18.6%;
Local Similarity 30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
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                                                                                                                                                                                                                 4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                      LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                                                                                                                                   LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
                                                                                    DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 142
VTPGKGSLVIHFSPPFD--
                                                                                                                                                                                                                                                              65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 20.0%; Score 214; DB 2; Similarity 30.5%; Pred. No. 1.4e-11; 60; Conservative 39; Mismatches 86
                                                                                                                                                                                                                                                              Conservative
-VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                          38; Mismatches
                                                                                                                                                                                                                                                                                Score 199; DB 2
Pred. No. 3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFN-gamma R species-specific cofactor; t
                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 325;
                                                                                                                                                                                                                                                                                                         Length 332,
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                32;
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                                                                                                                                                                                                                                                              Gaps
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  197
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R:Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S. Cell 76, 793-802, 1994

A;Title: Identification and sequence of an accessory factor required for activation of t A;Reference number: A49946; MUID:94170380

A;Reference number: A49946; MUID:94170380

A;Molecule type: mRNA
A;Residues: 1-337 <RES>
A;Cross-references: EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463550

A;Experimental source: clone pSK1
A;Accession: 138501
A;Molecule type: mRNA
A;Residues: 1-63,'0',65-337 <RES>
A;Cross-references: EMBL:U0587; NID:9463551; PIDN:AAA16956.1; PID:9463552
A;Cross-references: EMBL:U0587; NID:9463551; PIDN:AAA16956.1; PID:9463552
A;Cross-references: EMBL:U0587; NID:9463551; PIDN:AAA16956.1; PID:9463552
A;Experimental source: clone pJS3
C;Genetics: 21
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                        interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Fe
C;Accession: A31555
R;Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280; 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon gamma receptor accessory factor-1 precursor - human
c;Species: Homo sapiens (man)
C;Date: 16:Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.
A;Gene: GDB:IFNGR1; IFNGR
A;Cross:references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembran
                                                                                                                A;Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915 C;Genetics:
                                                                                                                                                                                                       A;Title: Molecular cloning and expression A;Reference number: A31555; MUID:89003065 A;Accession: A31555
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                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-489 <AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 GPPE-NIEVTPGEGSLIIRFSSPEDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 NCTQITATECDFTAASPSAGFPMDFNV----TLRLRAELGALHSAWVTMPWFQHYRNVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEKENT-SSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSK-----WFTADIMSIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
  cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 144; DB 2;
Pred. No. 2.3e-05;
9; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                28-Feb-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
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                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 337;
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                                                                                                                                                                                                                                                     interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                       receptor
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hypothetical protein ZK617.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 4
A; Introns: 10/3; 61/3;
144/3; 6683/3; 6768/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-6831 <WT2>
A;Cross-references: EMBL:273899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
A;Experimental source: clone ZK829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-6831 <WIL>
A;Residues: 1-6831 <WIL>
A;Cross-references: EMBL:273897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A;Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, May 1996
A;Reference number: Z20442
A;Accession: T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, A; Reference number: 220458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T27934; T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: ZK617.la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status:
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.1%;
Best Local Similarity 22.8%;
                                                                                                                                                                                                                                                                                                            1856 LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV 1912
                                                                                                   1963
                                                                                                                                                                                                      1913 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT------ 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 QCQLAIPVSSLNSQYCVSAEGVL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 YSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 DIFHPSVFVNGDEQEVDYDPETTCY;RVYNVYVRMNGSEIQYKILTQK-----EDDCDEI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 NFSSLKLNVYEEIKLRIRA---EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                                                                         4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NLKSPOKVEVDIIDDNFILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC 61
VIEKKGKHGRDWQ
                                                CLKVKAALLTSWK 185
                                                                                                                                                                                                                                                    TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary: translated from GB/EMBL/DDBJ
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                                                                                                                                                IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY 172
                                                                                                                                                                                                                                                                                                                                                                                                               44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                   GTPDVVDWDADRVS
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3 6800/3
  2006
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                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 97.5; DI
Pred. No. 15;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                   -LEWEPPKSDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6831;
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A:Map position: IV
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60
152/3; 669/3; 6776/1; 6808/3
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; serine/th
F:806-898, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2066-2158, 2358-2450, 2
96-5790, 6263-6356, 6386-6478, 5541-6635, 6649-6742, 6745-6838/Region: motif 2
F:1274-1372, 1373-1473, 1568-1570, 1671-1776, 1865-1964, 1965-2065, 2159-2258, 2259-2357, 2451-2
23, 4215-4313, 4314-4415, 4416-4516, 4612-4710, 4711-4811, 4908-5009, 5010-5109, 5110-5210, 5399-7
F:5940-6197/Domain: protein kinase homology <KINP
F:5948-5956/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 
C; Accession: 557242; S07571; S06797; S57218
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A;Title: Additional sequence complexity in the muscle gene, unc-22, A;Reference number: S57218; MUID:93387664
A;Accession: S57218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,'I'
A; Cross-references: EMBL:X15423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Sequence of an unusually large protein A; Reference number: S06797; MUID: 90044042 A; Accession: S06797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-6839 <BEN1>
A;Cross-references: EMBL:L10351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Benian, G.M.; L'Hernault, S.W.; Morris, M.E. submitted to the EMBL Data Library, February 1993
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A; Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Benian, G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November A;Reference number: S07571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: var. Bristol
R;Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
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                                                                                                                                                                                                                  Matches
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Residues: 792-6839 <BEN2>
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Best Local :
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     1921
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                                                                                                                                                          LKSPOK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYOK--TGMDNWIKLSGCQNI 56
                                                  TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                          LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV: 1920
KDTKAHIDGLKKG---QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT---
                                                                                                                                                                                                                  44:
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                 Lys #status predicted
                                                                                                                                                                                                                                   9.1%;
22.8%;
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                                                                                                                                                                                                                22;
                                                                                                                                                                                                             Score 97.5; Di
Pred. No. 15;
22; Mismatches
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C;Accession: T29585
R;Gattung, S.; Scheet, P.; Kemp, K.
R;Gattung, S.; Scheet, Data Library, November
submitted to the EMBL Data Library, November
A;Description: The sequence of C. elegans cos
A;Reference number: Z20647
A;Accession: T29585

translated

from

GB/EMBL/DDBJ

cosmid F55F8

hypothetical protein F55F8.3 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

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hypothetical protein ZK617.lb - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T27935; T28031
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T27935
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A; Introns: 10/3; 61/3; 1
3067/1; 3141/3; 3269/1;
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A; Residues: 17160 <WI2>
A; Cross-references: EMBL: 273899; P:
A; Experimental source: clone ZK829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T28031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: ZK617.1b
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A;Cross-references: EMBL:Z73897;
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Best Local Similarity
Matches 44; Conserv
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2323
                                                                              2292
                                                                                                                                                                                                                                      2185 LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP---CAKV 2241
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                                                                                                                                                          2242 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT------
                                                                                                                116
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                                    173 CLKVKAALLTSWK 185
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                                                                                                                                                                                            57 TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                      4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 56
                                                                                                                IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY 172
VIEKKGKHGRDWO 2335
                                                                            -----GTPDVVDWDADRVS-----LEWEPPKSDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GTPDVVDWDADRVS-----LEWEPPKSDGG----
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 6473/3; 7012/3; 7097/1; 7129/3
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Pred. No. 15;
22; Mismatches
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                                                                                                                                                                                                                                                                                                                Gaps
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187

WKASSTGKKKATTN--TNGFLIDVDKGENYCFHVQAVIL-SRRVNQKSPESPIKCT

239

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A; Molecule type: DNA
A; Residues: 1-925 <GAT>
A; Cross-references: EMBL: U80447; PIDN: AAB37807.1; GSPDB: GN00019; CESP: F55F8.3
A; Experimental source: Strain Bristol N2; Clone F55F8
C; Genetics:
A; Gene: CESP: F55F8.3
A; Map position: 1
A; Introns: 6/3: 44/2; 76/1; 109/2; 159/2; 204/3; 327/1; 469/3; 617/1; 775/1; {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g241439
A; Experimental source: adrenal gland
A; Experimental source: adrenal gland
A; Note: part of this sequence, including the amino end of the mature protein, was confir
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C:Superfamily: tissue factor
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F:1-35/Domain: stracellular *status predicted <SIG>
F:36-248/Domain: extracellular *status predicted <EXT>
F:36-248/Domain: extracellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 22-Jun-1999
C;Accession: J01319
R;Takayenoki, Y:; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: J01319; MUID:92109720
A;Accession: J01319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;249-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Domain: intracellular #status predicted <INT>
F;272-292/Domain: intracellular #status predicted <INT>
F;473-292/Domain: intracellular #status predicted f;81-89,215-238/Disulfide bonds: #status predicted
F;118.124/Binding site: carbohydrate (Thr) (covalent) #status predicted
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A; Residues: 1-292 <TAI
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132 YLETNLGQPTIQSFEQVGTKLNVTVQDARTLVR-----ANSAFLSLRDVFGKDLNYTLYY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                     44 MDNWIKLSGCONITSTKCNFS-SLKLNYYEEIKLRIRAEKENTSS------WYEVDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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R;Cofano, F.; MOULE, J. 1990
J. Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis,
A;Title: Affinity purification, peptide analysis,
A;Title: Affinity purification, peptide analysis,
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A; Residues: 1-94, E; 96-477 <GRA>
A; Cross-references: GB:M26711; NID:g194126; PIDN:AAA37896.1; PI
R; Hemmi, S.; Peghini, P.; Metzler, M.; Merlin, G.; Dembic, Z.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A; Title: Cloning of murine interferon gamma receptor cDNA: expr
A; Reference number: A34508; MUID:90099370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-94, E; 96-477 <HEM>
A; Residues: 1-94, E; 96-477 <HEM>
A; Cross-references: GB: MZ8233; NID: g194131; PIDN: AAA37898.1;
R; Munro, S; Maniatis, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
A; Title: Expression cloning of the murine interferon gamma re
A; Reference number: A36224; MUID: 90083245
A; Accession: A36224; MUID: 90083245
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A;Title: Cloning and expression of the CDNA for the murine in A;Reference number: A34423; MUID:90046824
A;Accession: A34423
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C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change
C;Accession: A34368; A34568; A34508; A34508; A36224; I48941
R;Kumar, C.S.; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.
J. Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular characterization of the murine interferon gam
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A;Accession: A34368
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M28995; NID:g194123; PIDN:AAA37895.1; PID:g309329 R;Raval, P.; Obici, S.; Russell, S.W.; Murphy, W.J. Gene 154, 219-223, 1995
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A; Residues: 1-477 <COF>
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A; Residues: 1-477 < KU
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A; Residues: 1-28 < RES>
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A; Residues: 10-477 < MUN>
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.; Aguet, M.
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D INR1_BOVIN STANDARD; PRT; 560 AA.

C Q04790;
T 01-CCT-1993 (Rel. 27, Created)
T 01-FEB-1994 (Rel. 28, Last sequence update)
T 01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-FINI IFNAR1 OR IFNAR.)
S INTERFERON- C EUVARTUS (BOVINE).
S Bos taurus (Bovine).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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MEDLINE; 93076908.
MEDLINE; 93076908.
MOUCHEI-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
MOUCHEI-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
"Specific antiviral activities of the human alpha interferons
determined at the level of receptor (IFNAR) structure.";
FEBS Lett. 313:255-259(1992).
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RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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"Cloning and characterization of a bovine alpha interferon receptor.";

Biochim. Biophys. Acta 1173:314-319(1993).

1 FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                         NLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN
LRLQSRVGCYSPVYCINTTERHKV
                          LLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                  NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN
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CYTOPLASMIC (POTENTIAL).

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Pred. No. 4.6e
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01-NOV-1997 (Rel. 35, L
15-FEB-2000 (Rel. 39, L
INTERFERON-ALPHA/BETA F
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"Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and pregnancy.";

Endocrinology 138:4757-4767(1997).

-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEIN SUBULTING THATS THATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovidae;
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                                                                 CARBOHYD
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"Structure of an ovine
                                                                                                                                                                                                                                                     PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                       SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINE
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINE
CONCEPTUS AT DAY 15 OF PREGNANCY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOM
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY
                                                                                                                                                                                                                                                            X95939; CAA65183.1;
U65978; AAB84231.1;
                                                                                                                                                                                                                                                                                         non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinol.
                                                                                                                                                                                                                  Transmembrane; Glycoprotein; Signal.

1 24 BY SIMILARITY.
25 560 INTERPERON-ALPHA/BETA RECEPTOR ALPHA
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Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
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CYTOPLIASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2090 (Rel. 39, Last annotation updat
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN
IFNARI OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in homospecific or heterospecific background.";
Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PRO
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BET
SUBUNITS THEMSELVES.
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uze G., Lutfalla G., Bandu M.T., Proudhon D., "Behavior of a cloned murine interferon alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
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                                                                                                                                                                                                                                                     EMBL; M89641; AAA37890.1;
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POTENTIAL
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                              INTERFERON-ALPHA/BETA RECEPTOR
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No. le-54;
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Best Local Similarity 51.0
Matches 104; Conservative
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01-FEB-1995 (Rel. 3
01-OCT-1996 (Rel. 3
CYTOKINE RECEPTOR (
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Q08334;
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EMBL; 217227; CAA78933.1; -.
EMBL; 008988; AAA86872.1; -.
PIR; A47003; A47003.
HSSP; P13726; 1DAN.
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                           J. MOI. EVOI. 41:338-344(1995).
-- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 96054036.
Lutfalla G., McInnis M.G.,
                                                                                                                                                                                                                                                                                                            rutfalla G., Gardiner K., Uze G.;
"A new member of the cytokine receptor
21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                              TISSUE-FETAL BRAIN; MEDLINE; 93300510.
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                                                                           entities requires a
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                                                            equires a license agreement (See http://www.isb-sib.email to license@isb-sib.ch).
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31, Last sequence update)
34, Last annotation update)
CLASS-II CRF2-4 PRECURSOR.
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Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
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6; Mismatches 63;
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P38484;
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DOMAIN
                                 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
1NTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                     _HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                              TISSUE-LUNG FIBROBLAST;
MEDLINE; 94170380.
                                                                                                                                                                SEQUENCE FROM N
                                                                                                                                                                                                             IFNGR2 OR IFNGT1
                                                                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                                                                                                                                         TSWKIGVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                            KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                             -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI
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                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Mammalia;
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A -> D (IN REF. 2).

FLGHP -> VGRME (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).
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Pred. No. 4.2e
99; Mismatches
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BY SIMILAR
POTENTIAL.
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                   Hominidae;
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No. 4.
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Matches 56
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CARBOHYD
CARBOHYD
  DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS. MEDILINE; 93183911.

Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gar "Alignment of disulfide bonds of the extracellular domain interferon gamma receptor and investigation of their role biological activity.";
                                                                                                                                                                                                                                                                                                                                                                      INGR_HUMAN STANDARD; PRT; 489 AA p15260; p1-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed, entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              MEDLINE; 89003065.
                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                         IFNGR1.
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                                                                                                                                                                                                        Aguet M., Dembic 2.,
                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                   Molecular cloning and
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                                                                                                                                              55:273-280(1988).
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18C61B10AD90E509 CRC64;
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                                                                Garotta
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Matches 45
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Sogabe S., Stuar ...
Winkler F.K., Robinson J.A.;
Winkley F.K., Robinson J.A.;
Win
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                      98
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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FUNCTION: RECEPTOR FOR
INTERFERON-GAMMA DIMER.
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                                                                      NISDHVGDPSNSLWVRVKARVGQKE--SAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMI
                                                                                                                                                               SVPTPTNVTIESYNMNPIVYWEY--QIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYC
                                                                                                               NFSSLKLNVYEEIKLRIRA---EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI 118
                                                                                                                                                                                                                                                         1 Similarity 22.1
45; Conservative
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., Stuart F.,
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                                                                                                                                                                                                                                                                                                                                                                          54404
                                                                                                                                                                                                                                                                              10.48;
--SPGTK-----DSVMMALDGLSFTYSLLIWKNSSGVEERIENI 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the extracellular interferon gamma receptor
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                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
DCF9E574D8F47400 CRC64;
                                                                                                                                                                                                                                                      Score 111; DE
Pred. No. 0.01
11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERFERON-GAMMA RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce,
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RESULT
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DT 01-J
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PWP2_CAEEL
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Best Local Similarity
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TF_BOVIN
P30931;
01-JUL-1993
01-JUL-1993
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWP2_CAEEL P91341;
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15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gattung S., Scheet P., Kemp K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: CONVAINS 6 WD REPEATS (TRP-ASP DOMAINS).
-i- SIMILARITY: BELONGS TO THE PWP2 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U80447; AAB37807.1; -. WORMPEP; F55F8.3; CE11192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F55F8.3
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                              Hypothetical
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
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                                                                                                                                      LSISPSGYHLLASDERGVVHFVHLLSEFKIYTFRSNKPIGSLQWSPDATRVAICRENDLQ
                                                                                                                                                      AQIGPPEVHLEAEDKAIVIHI---------
                                                                                                                                                                                                   MDNWIKLSGCQNIT--STKCNFSSLKLNVYEEI--KLRIRAEKENTSSWYEVDSFTPFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QCQLAIPVSSLNSQYCVSAEGVL
                                                                                                                                                                                   MDTNFKLSNCIGTVYRDGQVAFSKDGYSVISPIGNKLSIFDLRNNTSKTLDIDCNYNIKR
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                                                                                           IHEFGKSIENKVYNPFSLSRTYKLSSDS
                                                                                                                                                                                                                                  38;
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                                                                                                                                                                                                                                8.9%;
nilarity 25.7%;
Conservative 1:
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(Rel. 36, Last sequence update)
(Rel. 36, Last annotation updat
YPTOPHAN PROTEIN % HOMOLOG.
                                                                                                                                                                                                                                                                                                    1 protein;
188 218
358 388
400 430
486 514
524 554
 (Rel.
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 26,
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18 WD1.
88 WD2.
80 WD3.
14 WD4.
54 WD5.
 Created)
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 sequence update)
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                                                                                                                                                                                                                                Score 95.5; DB 1;
Pred. No. 0.64;
9; Mismatches 70;
                                    PRT;
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                                                                                                                                                                                                                                 70;
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INGR_MOUSE
ID INGR_M
AC P15261
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Best Local
 INGR_MOUSE
P15261;
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LIPID
SEQUENCE
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CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOY-1997 (Rel. 35, Last annotation update)
TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00346; TISSUEFACTOR, PROSITE; PS00621; TISSUE_FACTOR; 1.
PFAM; PF01108; Tissue_fac; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-ADRENAL GLAMEDLINE; 92109720.
                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                    187
                                                                                          144 WK-NSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 198
                                                                                                                 132
                                                                                                                                                             74
                                                                                                                                                                                   44 MDNWIKLSGCQNITSTKCNFS-SLKLNVYEEIKLRIRAEKENTSS------WYEVDSFTP
                                                                                                                                    FRKAQIGPP-----EVHLEAEDKAIVIHISPGTKDSVMWALD---GLSFTYSLLI 143
                                                                    WKASSTGKKKATTN--TNGFLIDVDKGENYCFHVQAVIL-SRRVNQKSPESPIKCT
                                                                                                                YLETNIGQPTIQSFEQVGTKLNVTVQDARTLVR----ANSAFISIRDVFGKDLNYTLYY
                                                                                                                                                             LGNW--KNKCFYTTNTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24055;
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                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                           Conservative
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             STANDARD;
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274
32475
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292
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153
181
181
89
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22.7%;
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POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PALMITATE (BY SIMILARITY).

FE471D92BFBCE163 CRC64;
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Pred.
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WKS MOTIF.
POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
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             PRT;
                                                                                                                                                                                                           Mismatches
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No. 0.
             477
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oved. Usage by and for commen
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/.28;
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                                                                                                                                                                                                                                 Length 292;
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31;

Gaps

9

96

131

239

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Appella E:

Appella E:

*Affinity purification, pepular

mouse interferon gamma receptor.";

mouse interferon 265:4064-4071(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJUE: 90099370.

MEDIJUE: 90099370.

MEDIJUE: 90099370.

Hemmi S., Peghini P., Metzler M., Merlin G., Dembic Z., Aguet M.; "Cloning of murine interferon gamma receptor cDNA: expression in human cells mediates high-affinity binding but is not sufficient confer sensitivity to murine interferon gamma"; Proc. Natl. Acad. Sci. U.S.A. 86:9901-9905(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERFERCE
IFNGRI OR IFNGR.
MUS musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990
01-AUG-1990
15-JUL-1999
                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
  EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-28 FR
MEDLINE; 95197006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray P.W., Leong S., Fennie E.H., Fernandez-Luna J., Schreiber R.D., "Cloning and expression of the cDI receptor.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR.
                                                                       or send an
                                                                                                                                                                                                                                                                                  mouse interferon-gamma receptor.
Gene 154:219-223(1995).
                                                                                                                                                                                                                                                                                                                             Raval P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 90154099.
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Mariano T.M., Pestka S.;
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                                                                                                                                                                                                                                                                                                             *Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cofano
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Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Biol.
                                                                                                                                                                              FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE INTERFERON-GAMMA DIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 M28995;
M26711;
M28233;
M25764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S., Maniatis T.;
ession cloning of the
Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90046824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem.
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                                                                                                                                                                                                                                                                                                                             Obici S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore S.K.,
                                                                      email to license@isb-sib.ch).
AAA37895.1; ALT_INIT.
; AAA37896.1; -.
; AAA37898.1; -.
; AAA39177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264:17939-17946(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sci.
                                                                                                                                                                                                                                                                                                          Russell S.W., Murphy W.J.; f the 5' flanking region an
                                                                                                                                                                                                                                                                                                                                                                                               receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine interferon gamma receptor cDNA.";
.A. 86:9248-9252(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frost
                                                                                                                                                                                                                                                                                                                                                                                                                                        S., Yuhki N.,
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Best Local S
Matches 46
                                SEQUENCE FROM N.A.
TISSUE-LYMPHOCYTES;
MEDLINE: 88061067.
Streuli M., Hall L.R., Saga Y., Sch
"Differential usage of three exons
mRNAs encoding human leukocyte comm
J. Exp. Med. 166:1548-1566(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J05265; AAA39178.1
EMBL; U05960; AAA80980.1
PIR; A34368; A34368
PIR; A34423; A34423.
PIR; A34508; A34508.
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PIR; A34423, A34423.
PIR; A34508; A34508.
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DOMAIN
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Eukaryota; Metazoa; C
Eutheria; Primates; C
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01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-197 (Rel. 35, Last annotation updat
LEUKOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.)
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P08575;
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l Similarity 23.4%;
46; Conservative
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                                                                          Saga Y., Sch
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BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                          Y., Schlossman S.F., Saito e exons generates at least f
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Pred. No. 0.57
3; Mismatches
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 (EC 3.1.3.48) (L-CA) (CD45 ANTIGEN)
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                                   CARBOHYD
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CARBOHYD
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DOMAIN
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Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00700; PRTYPHPHTASE.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y00638; CAA68669.1; HSSP; P18052; 1YFO. MIM; 151460; -.
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Streull M., Krueger N.X., Thai T., Tang M., Saito H.;

"Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and
                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                      Alternative
                                                                                                                                                                                                                                                                                                                                PFAM; PF00102; Y_phosphatase;
Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGENESIS
                       CARBOHYD
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                           SIGNAL
             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHICH ARISE BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD45 entry;
WWW-"http://www.ncbi.nlm.n1h.gov/prow/cd/cd45.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O J. 9:2399-2407(1990).

FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN RECEPTOR. THE FIRST PYPAGE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE THE FIRST ONE.

CATALLYIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O - PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF
                                                                                                                                                                                                                                                                                                                                                       PF00041; fn3; 2
 splicing;
                                                                                                                                                                            1304
575
597
1304
479
571
919
1235
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851
 78
90
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POTENTIAL.
                                                                                                                                                                C->S: LOSS POTENTIAL.
                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (POTENTIAL).
FIBRONECTIN TYPE-III (POTENTIAL).
PROTEIN TYROSINE PHOSPHATASE.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                   phosphorylation;
ase; Signal.
                                                                                                                                                                                                                                                                      EXTRACELLULAR POTENTIAL.
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RESULT
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Query Match
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P26690;
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
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SEQUENCE
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-).
Glycine max (Soybean).
Eukaryota; Viridiplannae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudlootyledons;
core eudloots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
                                                                                       HSSP: P14550; ZALR.
PRINTS; PRO0069; ALDKETRDTASE.
PROSITE; PS00062; ALDKETO_REDUCTASE_3;
PROSITE; PS00063; ALDKETO_REDUCTASE_1;
PROSITE; PS00798; ALDKETO_REDUCTASE_1;
                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                 Welle R., Schroeder G., Schiltz E., Grisebach H., Schroeder J.;

"Induced plant responses to pathogen attack Analysis and
heterologous expression of the key enzyme in the biosynthesis of
phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63).",

Eur. J. Biochem. 196:423-430(1991).

-!- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF
4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF
GLYCEOLLIN TYPE PHYTOALEXINS.
-!- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
PHYTOALEXINS IN SOYBEAN.
                                                                                                                                                                        EMBL; X55730; CAA39261.1; -. PIR; S14222; S14222.
                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: MONOMER.
-!- INDUCTION: BY PATHOGEN ATTACK.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. HAROSOY
MEDLINE; 91177016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine.
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                                                                             PFAM;
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                                             PF00248; aldo_ket_red; 1.
noid biosynthesis; Oxidoreductase; NADP.
NCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529
1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 90.5; D; Pred. No. 2.8; 23; Mismatches
Score
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 90;
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                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                         Usage
 Length 315
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                                                                                                                                                                                                                                                         γď
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        DOMAIN
TRANSMEM
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REPEAT
REPEAT
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INR2_BOVIN
095141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC)
(TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-
                                                                                                                                                                                                                                                            entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.; "Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                CHAIN
                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pregnancy.";
Endocrinology 138:4757-4767(1997).
-!- FUNCTION: RECEPTOR FOR INTERFERONS
-!- FUNCTION: TOWNER. TRANSDUCTION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                  EMBL; U75304; AAB84233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 98006426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFNAR2 OR IFNARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265
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                                                                                                                                                                                                                                                                                                                                                                                    KINASE, JAK1.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYDKERMNQNLHIFDWALTEQDHHKISQISQSRLISGPTKPQLADLW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRKGASRGPNEVMENDVLKEIAEAHGKSI-----AQVSLRWLYEQGVTFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRK-AQIGPPEVH------LEAEDKAIVIHISPGTKDSVMWALD-GLSFTYSLLIWKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGLTKAIGVSNFSVKKLQNLLSVATIRPVVDQVEMNLAWQQKKLREFCKENGIIVTAFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITSTKC----NFSSLKLN------VYEEIKLRIRAEKENTSSWYE-----VDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSLKTLQLEYLDL----YLIHWPLSSQP-GKFSFPIEVEDLLPFDVKGV--WESMEECQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFD----YQKTGMDNWIKLSGCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos.
                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
        246
267
367
362
362
230
230
                                                                                                                                                                                                              Glycoprotein;
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       BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                         CYTOPLASMIC |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.5:
8; Mismatches
                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                            INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                              rotein; Repeat; SIMILARITY.
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                                                                                          MIC (POTENTIAL)
TANDEM REPEATS
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INTERACTING WIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ξ
                                                                                                                                                                                                                                                                                             Usage by
                                                                                            REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                            Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HITH
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                                                                                          ဝှု
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                                                                                         S-L-E-D-
                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                  a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                            BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264
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     INRZ_HAMAN

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Matches
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Cohen B.,
Submitted
[5]
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INR2_HUMAN P48551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERPERON ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC)
(TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-
                                                                                                                                                                                                                                                                                                                                                                                receptor subunit generated by altern of a cytokine receptor gene cluster. EMBO J. 14:5100-5108(1995).
                                                       TISSUE-BLOOD;
                                                                     SEQUENCE FROM N.A.
                                                                                                         "Cloning and exp:
interferon alpha
J. Biol. Chem. 2'
                                                                                                                                                         Domanski P., Witte M., Kellum M., Rubinstein M., Pitha P., Colamonici O.R.;
                                                                                                                                                                                         SEQUENCE FROM N.A. (LONG MEDLINE; 95394915.
                                                                                                                                                                                                                                           Novick D., Cohen B., Ru
"The human interferon a
molecular cloning.";
Cell 77:391-400(1994).
                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (SHORT FORM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lutfalla G., Holland S.J., Cinato E., Rogers N.C., Smith J.M., Stark G.R., Kerr I.M., Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFNAR2 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutant USA cells are complemented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTK---DSVMWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF--ILRWNRSDESYGNVTFSFDYQKTGMDNWIK-LSGCQNITSTKCNFSSLKLNVYEEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEELQFYLAF -----IEEHAGNSVKRHQPQITGNITKNFNYVIDKLIPNTNYCISVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFQSVLSWELKNHSIVPTHYTLWYTIMSKREDMKVVKDCINVTRSFCDLTDVWVNTTDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPQVVGFRENAKLVICMGSFFLVPDKPLDPPEF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96067138.
                                                                                                                                                                                                                                                                                                              94236684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ens (Human).
; Metazoa; Chordata; Craniata; Vertebrata;
Primates; Catarrhini; Hominidae; Homo.
                     Kim S.H., (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530
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101
191
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                                                                                                                                       expression of a long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                       beta receptor that is required 70:21606-21611(1995).
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101 P
191 P
59584 MW;
                                                                     (LONG
                     Novick D., Rubinstein M.; ) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                           Rubinstein I
n alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
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                                                                     FORM).
                                                                                                                                                                                                           FORM),
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                                                                                                                                                                                                                                                                                                                                                                                                    by alternative
e cluster.";
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POTENTIAL.

POTENTIAL.

66A2C6D896B4DAD6 (
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Pred. No. 1.1;
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                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                                                                              3
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                                                                                                                                                                                                                                                                                                                                                AND
                                                                                                                                                                                                                                                                              receptor: characterization
                                                                                                                                       form
                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Monneron
Gardiner K
                                                                                                                                                                                                                                                                                                                                                PARTIAL
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                                                                                                                                       of the
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e processing of a
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                         Hackett
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Mogensen K.E.,
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                                                                                                                                       subunit of
                                                                                                                       signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530
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                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                    member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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48;

Gaps

10;

171

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THEWS

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"Soluble and membrane-anchored forms of the human IFN-alpha/Deta receptor.";
J. Leukoc. Biol. 57:712-718(1995).
-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG
                                           CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U29584
EMBL; X89772
MIM; 602376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISCUSSION OF VARIOUS FORMS, AND PARTIAL SEQUENCE MEDLINE; 95279874.
                                                                                                                                                                                                       DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                   IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG AND SOLUBLE FORMS ARE DIRECTLY INVOLVED IN SIGNAL TRADUCTION DUE TO THEIR INTERACTION MITH THE TYR KINASE, JAK1. THE LONG FORM ALSO INTERACTS WITH THE TRANSCRIPTIONAL FACTORS, STAT1 AND STAT2. BOTH FORMS ARE POTENT INHIBITORS OF TYPE I IFN ACTIVITY.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
ALTERNATIVE PRODUCTS: THREE ISOFORMS; A LONG FORM/IFNAR2-2 (SHOWN ALTERNATIVE PRODUCTS: THREE ISOFORMS; A LONG FORM/IFNAR2-3/P40; ARE PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPPORS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPPORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L42243;
L42238;
L42239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L41943
L41942
X77722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L42240;
L42323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L41944
                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JC
AAB46417.1; JC
AAB46417.1; JC
B; AAB46418.1; JC
G; AAB46419.1; JC
                                             27
2444
265
207
207
2116
1188
1192
238
240
281
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                                             243
264
515
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227
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1192
239
331
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JOINED.
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JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal; Alternative splicing;
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SA -> FS (IN ISOFORM 2-3).

MISSING (IN ISOFORM 2-3).

NEHNELAWDEPPLIPPLEAMDMVEVIISINRKKKVWDYNYDDE

SDSDTEMAPR -> RQCLAKGWNAVAHRCSHNALQSETPE

LKQSSCLSFPSSWDYKRASLCPSD (IN ISOFORM 2-
                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                        CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                         INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                           BETA
    밁
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Best Local S
Matches 46
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998
15-JUL-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I10R_MOUSE
Q61727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
    TRANSMEM
DOMAIN
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                    Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/announcer.com.arc.in.ch/sib.ch/announcer.com.arc.in.ch/sib.ch/announcer.com.arc.in.ch/sib.ch/announcer.com.arc.in.ch/sib.ch/announcer.com.arc.in.ch/sib.ch/sib.ch/announcer.com.arc.in.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch/sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-C57BL/6 X A. MEDLINE; 94068585.
                                                                                                                                                                                                                                                                               EMBL; L12120; AAA16156.1; -. MGD; MGI:96538; IL10RA.
                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERLEUKIN-10 IL10RA OR IL10R
                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206
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l Similarity 22.7%;
46; Conservative 2
                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332
10
151
515
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(Rel. 36, Last sequence update)
(Rel. 37, Last annotation updat
-lo RECEPTOR PRECURSOR (II-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          }.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515
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241
262
262
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225
113
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1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-HEMATOPOIETIC;
                                                                                                                                                                                                                                       Glycoprotein;
POTENTIAL
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  INTERLEUKIN-10 RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB
Pred. No. 1.2;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM 2-1).
F -> V (IN REF. 2 AND 4).
M -> V (IN REF. 3).
M -> V (TO REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
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1.2;
                                                                                                                                                                                                                                                            Signal
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Mus.
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a collaboration MBL outstation -

YBW

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                                                                                                                                                                                                                                                                                     Query Match 8.2%; Score 87.5; DB 1; Length 575; Best Local Similarity 20.0%; Pred. No. 1.8; Matches 47; Conservative 38; Mismatches 89; Indels 6
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
177 FSELKNATKRVKQETFTLTVPIGVRKFCVKVLPRLESRINKAEWSEEQCLLITTE 231
                    112 EDKAIVIHISPGTKDSV-MWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS--- 168
                                                                       123 VDEVIL-----TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQVFKDLRVYKISIRK 176
                                                                                                                                         23 GTELPSPSYVWFEARFFQHILHWKPIPNQSESTYYEVAL----KQYGNSTWNDIHICRKA 78
                                                                                                                                                                                                                                       1 GKNLKSPQKVEVDIIDDNFILRW----NRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNI 56
                                                                                                                                                                                                                                                                                                                                                                           575 AA; 64248 MW; 820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                                                     89; Indels 61; Gaps
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Search completed: June 1, 2000, 04:38:52 Job time: 14315 sec

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Result
No.
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Maximum DB seq length: 1000000
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Perfect score:
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   Score
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Match
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Gapop 10.0 , Gapext 0.5
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1072
1 GKNLKSPQKVEVDIIDDNFI........WKIGVYSPVHCIKTTVENEL 203
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(without alignments)
203.511 Million cell updates/sec
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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  Q10466
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Q61190
Q63953
Q9YGC8
Q14936
Q23020
Q23550
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Q9yhw0 gallus gall
Q61190 mus musculu
Q63953 mus musculu
Q63953 mus musculu
Q9ygc8 gallus gall
Q14936 homo sapien
Q23020 caenorhabdi
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Q23557 caenorhabdi
Q23571 mus musculu
Q5209 oryctolagus
Q88307 mus musculu
Q95209 oryctolagus
Q88307 mus musculu
Q15467 homo sapien
Q28733 oryctolagus
Q10466 saccharomyc
Q99105 saccharomyc
Q99105 saccharomyc
Q992673 homo sapien
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7.2	7.3	7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7
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P91305	090754	055203	055205	061210	P89031	001531	Q9XWD9	Q62319	035238	023854	035983	035663	Q9X257	023861	035664	094977	Q60705	Q94538	Q94537	Q08773	Q58863	070535	Q07784	Q58459
P91305 caenorhabd1	O90754 foot-and-mo	O55203 mus musculu	O55205 mus musculu	O61210 caenorhabd1	P89031 ovine papil	001531 caenorhabdi	Q9xwd9 caenorhabdi	Q62319 mus musculu	O35238 mus musculu	O23854 brassica ca	O35983 mus musculu	O35663 mus musculu	Q9x257 thermotoga	O23861 brassica ca	O35664 mus musculu	O94977 homo sapien	Q60705 mus musculu	Q94538 drosophila	Q94537 drosophila	Q08773 saccharomyc	Q58863 methanococc	rattus	Q07784 gallus gall	Q58459 methanococc

## ALIGNMENTS

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RESIDENT QEET QUE PROPERTIES ACCORDED TO QUE PRO
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                Q63953 PRELIMINARY;
Q63953;
Q1-NOV-1996 (TrEMBLrel. 01, C:
01-NOV-1996 (TrEMBLrel. 01, L.
01-NOV-1999 (TrEMBLrel. 12, L.
INTERFERON GAMMA RECEPTOR 2 ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O61190;
O61190;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
O1-NOV-1999 (TrEMBLrel. 12, MEMBER 4 (CLASS II CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CY ILlORB OR CRFB4 OR CRF2-4.
SEQUENCE FROM N.A.
STRAIN=129SV/J;
MEDLINE; 97128072.
EBENSPERGER C., RHEE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 97199375.
GIBBS V.C., PENNICA D.;
"CRF2-4: isolation of c
                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:109380; AAC53062.1; ...
MGD; MGI:109380; I110rb.
PFAM; PF00041; fn3; 1.
SEQUENCE 349 AA; 39774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins.
                                                                                                                                                            HEMMI S., BOHNI R., STARK G "A novel member of the interfunctionality of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 186:97-101(1997)
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                                                                                                                 76:803-810(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --HLSKYGDYTVRVRABLADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLHLRESAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNWIKLSGCQNITSTKCNFS
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                                                                                                                                                            STARK G., DI MARCO F., AGUET M.;
the interferon receptor family complements
e murine interferon gamma receptor in human
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  MUTHUKUMARAN
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Last sequence update)
Last annotation update)
(INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
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Pred. No. 7.4e-12;
3; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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LEMBO D.,
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Mus.
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Best Local S
Matches 53
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Matches 65
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O9YGC8;
O1-MAY-1999 (TIEMBLIEL 10, C
O1-MAY-1999 (TIEMBLIEL 10, L
O1-MAY-1999 (TIEMBLIEL 10, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1;
EMBL; AF082666; AAD13671.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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    79
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                                                                                                                                                                                                                                            PQKVEVDIIDDNFILRWNRSDESVGNVTFSFD----YQKTGMDNWIKLSGCQNITSTKCN
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    VSS--LSVYGAYVLRVRTEWEDEHSDWAVVRFKPMADTVIGPPSVNVKSESGTLHVDFTG
                                                                             FSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS- 122
                                                                                                                                                                        PRNARISSYNFRSVLLWDPPGVRKGNLSYTVQAKSIFPKQNFNN-----VTTNLNVTECD
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                                                                                                                                                                                                                                                                                                                                            Similarity 26.(
53; Conservative
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26.0%;
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                                                                                                                                                                                                                                                                                                                                            Score 179; DB
Pred. No. 1.3e
$5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Pred. No. 1.9e-10;
8; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBF24E9E CRC32;
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interferon/interleukin-10
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                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
.3e-08;
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RESULT 6
Q23020
PRELIMINARY;
ID Q23020
PRELIMINARY;
AC Q23020; Q27232;
DT 01-NOV-1996 (TremBLrel. 0)
DT 01-NOV-1996 (TremBLrel. 0)
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Best Local
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Q14936;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 97246734.
MERLIN G., VAN DER LEEDE B.-J.M., MCKUNE K., KN
BANNWARTH W., ROMQUIN N., VIEGAS-PEQUIGNOT E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The gene for the ligand binding receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89003065.
AGUET M., DEMBIC Z., MERLIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [mmunogenetics 45:413-421(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
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                                                                                                                                                                                      119 HISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (DEC-1994) to the L; U19247; AAC52064.1; J
L; U19241; AAC52064.1; J
L; U19242; AAC52064.1; J
L; U19243; AAC52064.1; J
L; U19244; AAC52064.1; J
L; U19245; AAC52064.1; J
L; U19246; AAC52064.1; J
L; U19246; AAC52064.1; J
UENCE 484 AA; 53818 M
                                                                                                                                                                                                                                                                                                                        NLKSPQKVEVDIIDDNFILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                         DI-----
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                                                                                                                                                                                                                             NISDHVGDPSNSLWVRVKARVGQKE--SAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMI 143
                                                                                                                                                                                                                                                             NFSSLKLNVYEEIKLRIRA----EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI 118
                                                                                                                                                                                                                                                                                                    SVPTPTNVTIESYNMNPIVYWEY--QIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYC
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40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            39;
 Created)
Last sequ
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Pred. No. 0.06
39; Mismatches
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                                                          PRT;
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                                                          6048 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 484;
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   RROCOS GETTO AC
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Best Local
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EMBL; Z73899; CAA98081.1; ALT_INIT.
EMBL; Z73897; CAA98081.1; JOINED.
HSSP; Q63450; 1A06.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 13; 13.
PFAM; PF000049; pkinase; 1.
PRINTS; PR00014; ENTYPEIII.
MYOS1n; Kinase
SEQUENCE 6048 AA; 668449 MW; 19
                                                                                                      Q23550;
Q1-NOV-1996 (TrEMBLrel. Q
Q1-NOV-1998 (TrEMBLrel. Q
Q1-NOV-1999 (TrEMBLrel. J
UNC-22 PROTEIN.
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BENIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
"Additional sequence complexity in the muscle gene, unc-22, and encoded protein, twitchin, of Caenorhabditis elegans.";
Genetics 134:1097-1104(1993).
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                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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                                                                                                                                                                                                     Q23550
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MEDLINE; 90044042.
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22.8%;
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                                    yda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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Pred. No. 12;
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Best Local Similarity
Matches 44; Conserv
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Q23551; O1-NOV-1996 (TIEMB
Q1-NOV-1999 (TIEMB
Q1-NOV-1999 (TIEMB
Q1-NOV-1999 (TIEMB
Q1-NOV-1999 (TIEMB
                                                                                         WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURRIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SOUNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
WHITE S.;
Submitted (MAY-1996) to the EMBL/
EMBL; 273899; CAA98082.1; -.
EMBL; 273897; CAA98082.1; JOINED.
EMBL; 273897; CAA98065.1; -.
EMBL; 273899; CAA98065.1; JOINED.
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Submitted
EMBL; Z738
EMBL; Z738
HSSP; P027
                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94150718. WILSON R., AINSCOU
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caehorhabditis.
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PFAM;
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                                                            SEQUENCE FROM N.A.
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273897; CAA98064.1; -.
273899; CAA98064.1; JOINED.
P02751; IFVA.
PF00041; fn3; 31.
PF00047; 19; 17.
PF000647; 19; 17.
PF00069; PKInase; 1.
PF00069; PKInase; 1.
PF00069; FNTYPEIII.
ENCE 6831 AA; 752579 MW; 0A66C338 CRC32;
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Pred. No. 14;
22; Mismatches
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HSSP; P02751; IFNA.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 17.
PFAM; PF00069; PK1nase; 1.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 7160 AA; 789211 MW; 1
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Q16614;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR
QCD45, LC-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 87275816.
RALPH S.J., THOMAS M.L., MORTO
"Structural variants of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                        antigen (CD45) gene.";
J. Immunol. 141:2781-2787(1988).
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EMBL; M23480;
EMBL; M23481;
EMBL; M23482;
EMBL; M23483;
EMBL; M23484;
EMBL; M23485;
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PFAM; PF00102; Y_bhosphatase; 2.
PRINTS; PR00700; PRTYPHPHTASE.
Signal; Alternative splicing; Hydrolase.
SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                       Mech. Dev. 0:0-0(1997).
EMBL; AF031816; AAC16739.1;
HSSP; P01130; 1AJJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 12, Last annotation update)
SORTILIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING PRECURSOR
                          Glycoprotein.
NON_TER
                                                              PFAM; PF00041; fn3; 4.
PFAM; PF00057; ldl_recept_a; 11.
PFAM; PF00058; ldl_recept_b; 5.
                                                                                                                               MGD; MGI:1202296; Sorll.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                  SUESENS U., FENGER U., Mech. Dev. 0:0-0(1997)
                                                                                                                                                                                                                                        HERMANS-BORGMEYER I., HAMPE W., SUESENS U., FENGER U., HERBARTH
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M23490;
EMBL; M23491;
                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (GP250) (FRAGMENT).
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P18052; 1YFO.
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36; Conserv
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1143 AA;
    2033
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AAD15273.
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    227305 MW;
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Pred. No. 6.1;
23; Mismatches
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                                                                                                                                                                                                                                        SCHINKE B., METHNER B., SCHALLER H.C.;
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    DC8108CD CRC32;
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RESULT OF THE PROPERTY OF THE 
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Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 32; Conserv
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Q95209;
Q95209;
O1-FEB-1997
O1-FEB-1997
O1-NOV-1999
                                                                                                                                                                                                                                                                                                                      1652 APQNLQLSLHGEEEGVIVGHWSPPTHTHGLIREYIVEYSRSGSKVWTSERAASNETEIK- 1711
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HSSP; P01130; 1AJJ.
PROSITE; PS01209; LDLRA_1; 10.
PFAM; PF00057; ldl_recept_a; 11.
PFAM; PF00058; ldl_recept_b; 4.
PFAM; PF00041; fn3; 5.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sorting receptor are present in a novel mammalian lipoprotein receptor family member."; J. Biol. Chem. 271:24761-24768(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96394640.
YAMAZAKI H., BUJO H., KUSUNOKI J., SEIMIYA K., KANA SCHNEIDER W.J., SAITO Y.;
"Elements of neural adhesion molecules and a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1474 NLQLSLNREEEGVILGHWAPPVHTHGLIREYIVEYSRSGSKMWASQRAASNSTEIK----
1809 LTAQTAY 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
SEQUENCE. 2213 AA; 247764 MW;
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                                                                                                                                                                                                                  1711 ---NLLVNTLYTVRV-AAVTSRGIGNWSDSKSITTVKGKAIPPPNIHIDNYDE-----
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                                                  166 LSPETTY 172
                                                                                                                                                               122
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                                                                                                                                                                                                                                                                 62 NESSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                              6 SPQKVEVDIIDDN---FILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC 61
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                                                                                                                                                            PGTKDSVMWALDGLSFTYSL------LIWKNSSGVEER----IENIYSRHKIYK 165
                                                                                                          -----NSLSFTLTVDGNIKVNGYVVNLFWAFDTHKQEKKTMNFQGSSVSHKVGN 1808
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7 (TrEMBLrel.
9 (TrEMBLrel.
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19.2%;
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Last sequence update)
Last annotation updat
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Pred. No. 1
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pred. No. 16;
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Best Local S
Matches 33
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PROSITE; PS01209; LDLRA_1; 10.
PFAM; PF00057; Idl_recept_a; 11.
PFAM; PF00058; Idl_recept_b; 5.
PFAM; PF00041; fn3; 4.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR002014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q15467;
Q15467;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
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01-NOV-1998
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                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurthoria: Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                    J. Leukoc. Biol. 57:712-71
-i- SIMILARITY: BELONGS TO EMBL; X89814; CAA61940.1;
                                                                                                                                                                                         MEDLINE: 95279874.

NOVICK D., COHEN B., TAL N., RUBINSTEIN M.;

"Soluble and membrane-anchored forms of the
                                                                                                                                                                                                                                                            TISSUE-BLOOD;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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    SEQUENCE
                                                                                       Receptor;
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nes 33; Conservative
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8 (TrEMBLrel.
9 (TrEMBLrel.
    239
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(TrembLrel. 01, Last sequence update)
(TrembLrel. 08, Last annotation update)
ALPHA/BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                           . 57:712-718(1995).
BELONGS TO THE CLASS
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Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
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19.2%;
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Last sequence update)
Last annotation update)
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Pred. No. 17;
33; Mismatches
                          CHAIN
                                          SOLUBLE IFN ALPHA/BETA
    9DA1F03E CRC32
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                                                                                                                             FAMILY
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                                            RECEPTOR
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Best Local S
Matches 46
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Best Local Similarity 25.5
                                                                                                          Q28733; Q28736; Q28738; Q28738; Q28738; Q28736; Q1-NOV-1996 (TrEMBLrel. 01, L 01-NOV-1999 (TrEMBLrel. 12, L TITIN (FRAGMENT)).
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Q99624;
Q1-MAY-1997
Q1-MAY-1997
Q1-NOV-1999
                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1996) to the EMEMBL; 049082; AAB47236.1; -. PFAB; PF01490; Aa_trans; 1. SEQUENCE 504 AA; 55772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
LATIF F., LERMAN M.,
Submitted (FEB-1996)
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
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01-MAY-1997 (TrEMBLIE1.
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TRANSPORTER PROTEIN.
SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LPIYTELKDPSKKKMQHIS-NLSIAVMYIMYFLAALFGYLTFYN--GVESELLHTYS---
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46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MINNA J., DUH F.M., KOONIN E., BADI to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%;
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12,
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                                                                                                                                    Last sequence update)
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Last sequence update)
Last annotation updat
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Pred. No. 4
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Nature 345:273-276(1990).

EMBL; X64696; CAA45937.1; -.

EMBL; X17329; CAA35207.1; -.

HSSP; P56276; 1TLK.

PFAM; PF00041; fn3; 50.

PFAM; PF00047; fg; 3.

Myosin; Muscle protein.

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SEQUENCE
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TISSUE-PSOAS MUSCLE;
MEDLINE; 9023853.
LABEIT S., BARLOW D.P., GAUTEL M., GIBSON T., HOLT J., HSIEH C.L.,
FRANCKE U., LEONARD K., WARDALE J., WHITING A., TRINICK J.;
"A regular pattern of two types of 100-residue motif in the sequence of titin.";
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STRAIN=CE12:
MEDLINE; 92258380.
LABEIT S., GAUTEL M., LAKEY A., TRINICK J.;
"Towards a molecular understanding of titin.";
EMBO J. 11:1711-1716(1992).
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LABEIT S.;
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375 VPVNKSAIPER-----RLKYQNLIPGHEYQFRVKA----ENEIGVGEP 413
                                          327
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                                                                                                                                                                                                                                                                                                                                                                                   60 KCNFSSLKLNVY--------EEIKLRIRAEKE----NTSSWYEVDSFTPF 97
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Search completed: June 1, 2000, 04:38:14 Job time: 14306 sec

A\_Geneseq\_36:Y04994 A\_Geneseq\_36:W56309 A\_Geneseq\_36:W22602 A\_Geneseq\_36:R47812

55.00 55.00 54.50

105 103 95 107

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! Sequence of amino acid tra Mycobacterium species prot Clas II S-receptor kinase Tylactone synthase ORF2 p

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A_Geneseq_36:R60610
A_Geneseq_36:W02084
A_Geneseq_36:W0297
A_Geneseq_36:R29171
A_Geneseq_36:R74148
A_Geneseq_36:R4336
A_Geneseq_36:W44336
A_Geneseq_36:W44336
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A_Geneseq_36:R74752
A_Geneseq_36:W59836
A_Geneseq_36:R20231
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A_Geneseq_36:R87511
A_Geneseq_36:R61117
A_Geneseq_36:R41227
A_Geneseq_36:R76075
A_Geneseq_36:R92399
A_Geneseq_36:R92518
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A_Geneseq_36:W93962
A_Geneseq_36:W52296
A_Geneseq_36:W07702
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Query: US-09-240-675-1_COPY_27_229
Query length: 203
Database: A_Geneseq_36:*
                                                                                                                                      A_Geneseq_36:R23784
A_Geneseq_36:W22776
A_Geneseq_36:R67755
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Database length: 23686106
Search time (sec): 60.370000
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A_Geneseq_36:R96994
A_Geneseq_36:W59912
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A_Geneseq_36:R28496
A_Geneseq_36:R42635
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A_Geneseq_36:R11958
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A_Geneseq_36:R71723
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A_Geneseq_36:R14487
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Tobamovirus movement protein. I
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Spliced-deleted interferon alpha/beta r
Soluble interferon-alpha/beta r
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seq_name: A_Geneseq_36:W21805
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 2; Fig 7; 46pp; English.

Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (W21805) is characterised by a new domain (S) which follows an cend-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrana domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. IFNAR clone is predicted from a cDNA clone (see also T73520) obtd. If from human myeloma U266 cells. Soluble, non-membrane bound IFNAR cplice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNS alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
    W21805 standard; Protein; 434
    W21805;
                                                                                                                                                                                                                                                                                               Abramovich C, Ratovitski E, Revel WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                 11-MAY-1995.
20-0CT-1994; 075977.
24-0CT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1997 (first entry)
Spliced-deleted interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spliced-deleted interferon alpha-receptor interferon alpha-receptor; IFNAR.
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alignment_block:
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                                 Percent Similarity:
                                            Quality:
Ratio:
                                 100.000
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                                 Percent Identity:
                                 : 67
: 0
: 100.000
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51 17

Align seg 1/1 to: W21805 from: 1 to:

434

CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100 34

17

AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150

101 34 50

AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA

Mycobacterium species protein

seq\_name: A\_Geneseq\_36:R14487

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seq_documentation_block:
ID R28495 standard; Prot
AC R28495;
DT 31-MAR-1993 (first e
DE Sequence of a soulble
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Ratio: 5.075
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R204-95;
R28495;
31-MAR-1993 (f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; 52pp; French.

The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
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R14487 standard; Pr
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Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey MG, Uze G,
WPI; 91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
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DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (030533), was incubated with oligos (330534 and 030535. RZ8496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: R28495
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R71723 standard; Protein;
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17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P. Gresser I, Lutfalla G, Meyer
23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
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WPI; 92-382110/46.
N-PSDB; Q30532.
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Interferon receptor; alpha-interferon; beta-interferon.
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                                                                                         Homo sapiens WC9507716-A.
                                                                                                                                                   IFN receptor extracellular domain.

IFN receptor; interferon receptor; interferon-alpha; interferon-beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                            R71723;
16-OCT-1995
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E03114. EP-402279

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alignment_block:
US-09-240-675-1_COPY_27_229 x R71723
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                                                                                                                                       11-MAY 1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV C
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
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N-PSDB; Q86457.
Compsn. of monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compan of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English. A recombinant soluble form of the human interferon class I protein extracellular domain, given in R71723, was expresse either E. coli or COS cell hosts. The protein was used to immunomodulatory monoclonal antibodies.
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon example 3; Fig 7; 46pp; English.
                                                                                     Abramovich C, Ratovitski E, WPI; 95-200634/27
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Spliced-deleted interferon
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Ratio: 5.075
Similarity: 100.000
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/note= "comprises amino acid residues 1-413
422-427 of transmembranal IFNAR"
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alignment_scores:
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                                                                                               13-OCT-1990; F00758.

20-OCT-1989; FR-013770.

A (CNRS ) CNRS CENT NAT RECH SCI.

I Mogensen KE, Uze G, Lutfalla G, Gresser I;

N-PSDB; 91-148740/20.

N-PSDB; 911701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              documentation_block:
               New human alpha-interferon receptor protein - useful for testin interferon agonists and in treatment or diagnosis Disclosure; fig 4, 30pp; French.
This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and disception for the testing of IFN agonists and for treatment and disception is the testing of IFN agonists and for treatment and disception is the testing of IFN agonists and for treatment and disception is the testing of IFN agonists and for treatment and disception is the testing of IFN agonists and for treatment and disception is the testing of IFN agonists and for treatment and disception is the testing of IFN agonists.
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                                                                                                                                                                                                                                                  W09105862-A.
                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                 Human alpha-interferon receptor protein.
Human alpha IFN; IFN agonists; antiviral;
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                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1991 (first entry)
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IFN agonists and for t
nd tumours. Antibodies
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US-09-240-675-1_COPY_27_229 x R11958
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09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
E1d P, Gresser I, Lutfalla G
Tovey MG, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
R14488 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
                                                                              The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
                                                                                                                                                                                                                                                                                                                                                                              WPI;
                           and can be used to treat autoimmune diseases or rejection. See also Q14239.
                                                                                                                                                                                                                        New water-soluble polypeptide(s) with affinity in beta used to treat e.g. lupus erythematosus, E aplastic anaemia, diabetes mellitus, rheumatoid Disclosure: Page 47; 52pp; French.
                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q14240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
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      See also
557 AA;
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458. .55
/label=
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Behcet's disease,
d arthritis, etc.
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seq_documentation_block:
ID R28496 standard; Prot
AC R28496;
DT 31-MAR-1993 (first e
DE Sequence of a soulbile
DE with a high affinity
Interferon receptor;
OS Synthetic.
PN W9218626-A.
PD 29-OCT-1992; WO-F0031
PF 17-APR-1991; F00318.
PF 17-APR-1991; WO-F0031
PR 17-APR-1991; WO-F0031
PR 17-APR-1991; WO-F0031
PR 17-APR-1991; WO-F0031
PR 17-APR-1991; WO-F0031
PT Tovey M, UZe G;
DR WPI; 92-382110/46.
PI Tovey M, UZe G;
DR WPI; 92-382110/46.
PF Tovey M, UZe G;
DR Tovey M, UZe G
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US-09-240-675-1_COPY_27_229
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                                                                                                                                       water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejection claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (030533), was incubated with oligos 030534 and 030535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind the law as a search of the complete receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
ELID P, Gresser I, Lutfalla G, Me
       IFN in the same way as antibodies so are immunosuppressants e.g. treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids. Sequence 577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
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Gaps:
Percent Identity:
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alignment\_scores:

Quality:

340.00 5.075 100.000

Percent Identity:

100.000

67

Ratio: Percent Similarity:

alignment\_block: US-09-240-675-1\_COPY\_27\_229 x R28496

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alignment_scores
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06-CCT-1993.

1 MAR-1992; 400902.

13 MAR-1992; EP-400902.

PA (EUDI-) LAB EURO BIOTECHNOLOGIE SA.

PAnoit P, Maguire D, Meyer F, Plavec I, Tomore Management (Maguire D).

Panoit P, Maguire D, Meyer F, Plavec I, Tomore M, Meyer F, Meyer F
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                                                                                                                                                                                                                                                        Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                           US-09-240-675-1_COPY_27_229 x R42635
                                                                                                Align seg 1/1 to: R42635 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis
Disclosure; Fig 3; 21pp; English.
Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1994 (first entry)
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/label- extracellular_domain
/note- "soluble, immunogenic form of IFN-R"
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alignment_block:
US-09-240-675-1_COPY_27_229 x R75356
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                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                      R75356 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-1995 (first entry) Human IFN receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9507716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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interferon-beta; monoclonal antibody; immunomodulato
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                                AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                           CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTC
AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA
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                                                              yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
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/label-
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Gaps: 0
Percent Identity: 100.000
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201

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51

ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67

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seq_name: A_Geneseq_36:W21804
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Ratio: 5.075
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) bisclosure; Fig 7: 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splicedeleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
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24-0CT-1993; IL-107378.
(YEDA) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU9475977-A.
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W21804;
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                                        51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
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                                                               AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                 ATGATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
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                                                                                                                                                  AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
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/label= Transmembrane_domain
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Gaps:
Percent Identity:
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seq_documentation_block:
ID w93941 standard; Prot
AC w93941 standard; Prot
AC w93941; breast;
DT 30-JUN-1999 (first e
DE Human brx protein; breast;
KW anti-cancer; anti-prot
KW tumour suppressor; ov
KW immune tissue; prever
OS Homo sapiens.
PN w0991544-Al.
PD 01-APR-1999; U19782.
PR 23-SEP-1998; U19782.
PR 23-SEP-1997; US-05966
PR (DRIG/) DRIGGERS P H
PA (RUBL/) RUBLNO D M.
(SEGE/) SEGERS J.
PR Driggers PH, Rubino I
DR WPI; 99-254688/21.
DR N-PSDB; X24044.
PT Breast cancer gene er
PT protein, brx
Claim 1b; Page 58-62.
CC This invention descr:
CC nuclear receptor-binc
CC conbear protiferative of cother proliferative of cother proliferative of cother proliferative diseases
CC Brx gene can be used
CC Droliferative disease
SQ Sequence 1429 AA;
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                                                                                                                                                                                           protein, brx

Claim 1b; Page 58-62; 69pp; English.

Claim 1b; Page 58-62; 69pp; English.

This invention describes a novel human breast cancer gene encoding a nuclear receptor-binding auxiliary protein, brx. The brx encoded protein has anti-cancer, anti-proliferative and mitogenic activity and acts as a transcription factor and tumour suppressor. Levels of expression of Brx can be detected using the primers, probes and antibodies (contained in the kit) to determine a predisposition to breast and ovarian cancer and other proliferative disorders of immune tissues. Vectors containing the Brx gene can be used for prevention and treatment of cancers and proliferative diseases of mammalian reproductive and immune tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brx protein; breast cancer; nuclear receptor-binding auxiliary protein; anti-cancer; anti-proliferative; mitogen; transcription factor; human; tumour suppressor; ovarian cancer; proliferative disorder; treatment; immune tissue; prevention; reproductive tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast cancer gene encoding a nuclear receptor-binding auxiliary
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23-SEP-1997; US-059621.
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                                 Ratio:
75.00
1.923
52.703
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      Percent
Identity:
74
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alignment_scores:
    Quality:
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                                                                               seq_name: A_Geneseq_36:W93962
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                                                                                                                                                                                                                                                          ....TATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGA 178
                                                                                                                               ArgLeuSerGln
                         Protein;
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Sequence of the control of the contr
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                                                                                                                                                          22-LAN-1998, U12455.
17-JUL-1996; US-683743.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
KOTENÓS SV. PESTKA S;
WPI; 98-110590/10.
N-PSDB; V19874.
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This invention describes a novel human breast cancer gene encoding a nuclear receptor-binding auxiliary protein, brx. The brx encoded protein has anti-cancer, anti-proliferative and mitogenic activity and acts as a transcription factor and tumour suppressor. Levels of expression of Brx can be detected using the primers, probes and antibodies (contained in the kit) to determine a predisposition to breast and ovarian cancer and other proliferative disorders of immune tissues. Vectors containing the Brx gene can be used for prevention and treatment of cancers and proliferative diseases of mammalian reproductive and immune tissues. Sequence 30 AA;
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   rejection
Claim 2; Page
This sequence
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23-SEP-1998; U19782.
23-SEP-1997; US-059621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRFB4 protein.

CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease; septic shock; immune response; organ rejection; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9915544-A1.
                                                                                             New recombinant DNA - comprises sequences encoding interleukin-10 and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
W09802542-A1.
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99-254688/21.
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WPI; 97-043139/04.
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Athanasiou MA, Beal GJ, Blair DG, Fisher RJ,
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Database sequences: 145308
Database length: 14437401
Search time (sec): 65.150000
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-Q-/cgn2_l/USPT0_spool/US99240675/runat_30052000_164312_24612/app_query.fasta.1
-Q-/cgn2_l/USPT0_spool/US99240675/runat_30052000_164312_24612/app_query.fasta.1
-DB-ISsued_Patents_AA -ORM-fratan -SUFFIX-modif.rai
-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-COAPEXT-0.000 -GAPEXT-10.000 -GAPEXT-10.000
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-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-blosum62 -TRANS-buman40.cdi -LIST-45 -DOCALIGN-200
-THR_SCORE-pct -ALIGN-15 -MODE-LOCAL -OUTEMT-pfs -NORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US99240675 -NCPU-6 -ICPU-3
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2_6/ptcdata/1/1aa/5A_COMB.pep:US-08-362-512A-2 + 54.00 104.70 22.57 632 65ptcdata/1/1aa/5A_COMB.pep:US-08-443-104-4 + 54.00 104.70 22.57 632 65ptcdata/1/1aa/5A_COMB.pep:US-08-442-859-4 + 54.00 104.70 22.57 632 65ptcdata/1/1aa/5A_COMB.pep:US-08-498-499-4 + 54.00 104.70 22.57 632 65ptcdata/1/1aa/5A_COMB.pep:US-08-701-846-2 - 54.00 101.25 24.62 90 62 65ptcdata/1/1aa/5A_COMB.pep:US-08-701-846-2 - 54.00 101.25 24.62 90 62 65ptcdata/1/1aa/5B_COMB.pep:US-08-701-846-2 - 54.00 101.25 24.62 90 62 65ptcdata/1/1aa/5B_COMB.pep:US-08-804-227C-14 + 53.50 84.33 42.80 67 62 65ptcdata/1/1aa/5B_COMB.pep:US-08-804-227C-8 + 53.50 84.32 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 42.82 4
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/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-552-142A-9
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-910-973-9 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                           101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
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alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-328-256-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-328-256-11
                                                                                                                                                    Align seg 1/1 to: US-08-328-256-11 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/328
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Reluction DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L. REGISTRATION NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                    CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                        ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BROWDY AND NEIMARK
9 Seventh Street, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ication US/08328256
                                                                                                                                                                                                                                                 : 340.00
: 5.075
: 100.000
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                                                                                                                                                                                                                                                   Percent Identity:
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100.000
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-2
                                                                                 alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-307-588-2
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                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                       ; MOLECULE TYPE: US-08-307-588-2
                                                                                                                                             Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                      Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
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INFORMATION FOR SEQ ID NO:
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20007
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: CYCTEM: PC-DOS/MS-DOS
COMPUTER: CYCTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
                                                                                                                                                                                                                                                                                                                                                                                              NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2021672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE ITITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/OF FILING DATE: 05-DEC-1994 NIOR APPLICATION DATA: APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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1 ATGATGGTCGTCCTGCGGCGCGCGACCCCTAGTGCTCGTCGCCGTGGG
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                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                           436 amino acids
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MAGUIRE, Deborah
                                                                                                                                                                                                                                                                                                                                                                                 (202)672-5399
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                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                               Percent Identity:
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alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-328-256-12
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                                                                                                       alignment_scores:
Quality:
                                                                                                                                                                                         ; MOLECULE TYPE: US-08-328-256-12
                                                            Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                  TELEFAX: 204-7.
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12.
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g_documentation_block:
Sequence 12, Applicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/328,256
FILLING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILLING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RATOVITSKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                 single
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3ER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edward
                                                                                                                                                                                                                                                                                                                                   12:
                                                                   Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
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                                                                       100.000
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10
                                                                     ; MOLECULE TYPE: US-08-328-256-10
                alignment_scores
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                                                                                                                                                                                          TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
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FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                        REGISTRATION NUMBER: REVEL-
REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER: 25
RELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C
                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s 67
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Quality:
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                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                        linear
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9 Seventh Street, N.W.,
                                                                                     protein
 340.00
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Length:
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 67
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-471-454-2
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Percent Similarity: 100.000
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Patent No. 5731169
                    INFORMATION FOR
                                                                                                                                          PRIOR APPLICATION NUMBER: US 07/9/
APPLICATION NUMBER: IS-JUN-1992
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/1
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E. 32.2(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
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                                                                                           REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                    TELEPHONE:
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                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
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200797 NIXN UR N FOR SEQ ID NO: CHARACTERISTICS:
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                                                                           (703) 816-4000
                                                                                                                                                                                         UMBER: FR 89/13770
20-OCT-1989
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                                                      816-4100
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                                                                                                                                                                                                                                                      US 07/900,642
                                                                                                                                  32,205
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Percent Identity: 100.000
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LENGTH:

amino acids

amino acid

linear

single

protein

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; STRANDEDNESS:
; TOPOLOGY: 1ii
; MOLECULE TYPE:
US-08-471-454-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORDPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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                                                                                                             APPLICATION NUMBER: US/O FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 22201-4714
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Ratio:
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5.075
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Percent Identity:
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alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-466-974-2
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Quality:
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Ratio: 5.075
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                     APPLICANT: MOGENSEN, Knu APPLICANT: UZE, Gilles APPLICANT: LUTFALLA, Geo APPLICANT: GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
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CORRESPONDENCE ADDRESS:
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                                                                                                        CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
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STRANDEDNESS: sir
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                                                                                                                                                                                            ADDRESSEE:
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5. 5886153
                                                                                                                                                                      E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
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linear
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Percent Identity: 100.000
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SOFTWARE: Patentin Release #1.0, Version #1.25

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alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-471-453-2
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Ratio: 5.075
Percent Similarity: 100.000
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                                                                                                                                                                     Sequence 4, Application US/08307588 Patent No. 5919453
APPLICANT: BENOIT, PATTICK
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL
TITLE OF INVENTION: INTERFERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-UN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200797 NIXN UR :NFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         201 A 201
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                   INFORMATION:
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(703) 816-4100
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                 MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
   INTERFERON
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Gaps: 0
Percent Identity: 100.000
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; MOLECULE TYPE: US-08-307-588-4
                                                   seq_documentation_block:
; Sequence 3, Application PC/TUS9414277
                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3
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Quality:
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Ratio: 5.075
Percent Similarity: 100.000
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                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/EP93/00770 FILING DATE: 30-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                            201 A 201
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                               ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
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GY: linear
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3000 K Street, N.W.,
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Aguet, Michel
Bohni, Ruth
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31-MAR-1992
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05-DEC-1994
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Percent Identity:
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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

TITLE OF INVENTION:

Hemmi, Silvio

Receptor Subunit Polypeptides

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alignment_block:
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                                                                                                                                                                                                       seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                              Sequence 4 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATIN (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/1427 FILING DATE: 07-DEC-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                               182 TTTCATTCGATTATCAA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
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                                                     APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADURESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Californ's
                                                                                                                                                                                                                                                                                                                                                                          17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GluAsnLeuLysProProGluAsnIleAsp***TyrIleIleAspAspAs 17
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                      heSerAlaGluTyrArg 39
                                                                                                                                                                                                                                                                                                                                                                        nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                              CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 181
                                                                                                                                                                  4, Application US/08683743
5. 5843697
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David A. Jackson, Esq.
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3.613
79.487
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-412A-7
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                                                                                                                                                                                                    seq_documentation_block:
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                                                                                                                                                                                 Sequence
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HYPOTHETICAL: I
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
NAME: Jackson MUMBER: 26,742
REGISTRATION NUMBER: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                              ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          184 TCATTCGATTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                          134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                  53 ThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                                                                                                36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                19 yMetValProProFroGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT...... 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:

    Application US/08469412A
    5856125

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-343-1684
                                                                                                 Blair, Donald G
                                                                                                                      Mavrothalassitis, George
                                     Athanasiou, Meropi A.
                                                           Beal Jr., Gregory J
                                                                              Fisher, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.50
1.922
59.259
Dionyssios N. The ERF Genetic Locus and Its Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/683,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 54
Gaps: 1
Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601-1-050
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INVENTION:

UMBER OF SEQUENCES:

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alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-469-412A-7
                                                                                                                                                                                                                                                seq_documentation_block:
    Sequence 64, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                          APPLICANT: WHITE, MORRIS F.
APPLICANT: SUN, XIAO JIAN
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               367 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                           383 aGlyGluLysAlaProGlyGly 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..543
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                       32 AGGGTCGTCGCGCCCAGGAGGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 TTCCACCTGCGGCTGCGGACAACACCCCATGGGCCCACGGCGACGAGCACT 33
ADDRESSEE: LANIA-
ADDRESSEE: LANIA-
CHORESEE: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/469,412A FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-317-310A-64
                                                                                                                                                                                                                        4, Application US/08317310A 5858701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 543 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                            LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.00
3.389
75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "murine ERF amino acid sequence
(first 8 amino acids from first exon not
included)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 24
Gaps: 0
Percent Identity: 45.833
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-317-310A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-317-310A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08323170B Patent No. 5733772
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B
FILING DATE: 13-CCT-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1045 oThrAlaGlySerSerMet.SerSerGluProGly 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williamson, Kim C.
APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 03-OCT-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                         94111-3834
                                                                                                                                                                                                                                                                        San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                              California
                                                                                                                                                                                                                                                                                           Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617)227-5941
                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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2.652
79.310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JDP-022
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1
51.724
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APPLICATION NUMBER:

US 08/010,409

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alignment_block:
_US-09-240-675-1_COPY_27_229 x US-08-323-170B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-252-626A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               836 Lys 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 GGAGCGATGAGTCTGTCGGGAAT...GTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         803 rCysPheGlu...GluMetIleProTyrAsnLysGluIleLysTrpAsnL 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACA 151
                    CURRENT APPLICATION DATA:
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ISOLATED DNA ITTLE OF INVENTION: Protooncogene NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 TCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCCTCA 101
                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                            STREET: P.O. Dre
CITY: Charlotte
STATE: No. 5585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 015280-113100US
                                                                                                                                            ZIP: 28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
APPLICATION NUMBER: US/08/252,626A
                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysGluAsnLysSerLeuGlyAsnLeuValAsnAsnSerValValTyrAsn 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGlyAspIleGlyGlyIleLeuPheProLysAsnIleLysSerThrTh 803
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08252626A
                                                                                                                                                                                                                                     P.O. Drawer 34009
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                                                                                                                                                                                                                                                                                                                                                                                                            Graham, Douglas K.
Dawson, Thomas L.
                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                 Mullaney, David L.
Snodgrass, Hiram R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Earp, Henry S
                                                                                                                                                                                                                                                           Kenneth D. Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 576-0200
                                                                                                                                                                                         5585269th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.00
1.844
62.745
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                                                                                                                                                                                                                                                                                                                                             Isolated DNA Encoding C-MER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-41, 261
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                                        Version #1.30
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alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-252-626A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-505-218-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-252-626A-2 from: 1 to: 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 4, Application US/08505218 stent No. 5914447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
APPLICANT: ARAYA,
APPLICANT: MOURAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 31,665
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEPAX:
                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/505,218
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 999 amino acids s
ATTORNEY/AGENT INFORMATION: NAME: KRAUS, ERIC J
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                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 ATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT.....GACAACTTTA 136
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                                         APPLICATION NUMBER: US/0 FILING DATE: 03-NOV-1995 CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                              TRANSGENIC PLANTS INCLUDING A HYBRID NUCLEIC ACID SEQUENCE, COMPRISING AN UNEDITED MITOCHONDRIAL GENE FRAGMENT FROM HIGHER PLANTS AND PROCESS FOR PRODUCING THEM
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REFERENCE/DOCKET NUMBER: 1169-013
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: TELECHONE: (703) 684-1111
: TELECHONE: (703) 684-1114
: INFORMATION FOR SEQ ID AND 124
: INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
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Query: US-99-240-675-1_COPY_27_229
Query length: 203
Database: PIR_63:*
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pir2:A42701
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-0-/cgn2_1/USPTO_spoo1/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-0-/cgn2_1/USPTO_spoo1/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-DB-PIR_63 -QFMT-fastan -SUFFIX-modil.rpr -GAPOP=12.000
-GAPEXT-4.000 -MINARCH-0.100 -LOOPEXT-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPOEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000 -YGAPOEXT-0.500
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flagellar protein required for hypothetical protein MJ0288 - whypothetical protein 2 - spiror s-locus-specific glycoprotein S potassium-transporting ATPase, novel cellular protein TSK8.180 hypothetical protein R07B5.3 -
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pir2:JC2100
pir2:A69763
pir2:T34338
       seq_documentation_block:
interferon alpha receptor
                                                                                                      seq_name: pir2:S27387
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A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Reywords: cytokine receptor; 9jycoprotein; transmembrane protein
C;Reywords: cytokine receptor; 9jycoprotein; transmembrane proteicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydra*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interferon alpha/beta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C;Accession: A32694; S17112
R;Uze, G; Lutfalla, G; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into mou:
A;Reference number: A32694; MUID:90124632
A;Accession: A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor gene.
A;Reference number: S17112
A;Accession: S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross-references: EMBL:X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_27_229 x A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: A32694 from: 1 to: 557
                                                                                                                                           101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                    57.50
57.50
57.50
57.50
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115
114
113
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39.04
39.48
39.62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
0
100.000
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386
454
478
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H+-transporting ATP synth
homoserine dehydrogenase I
hypothetical protein M03D
       67
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                                                                                                                                           150
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type 1

precursor

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A:Experimental source: lung
A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:1-24/Domain: signal sequence #status predicted type 1 #status pred
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Blochim. Biophys. Acta 1173, 314-$19, 1993
A;Title: Cloning and characterization of a bovine alpha inte A;Reference number: S33770; MUID:93305725
A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S3770
R:Mouchel-Vielh, E: Lutfalla, G: Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                        interferon alpha/beta receptor - mouse C:Species: Mus musculus (house mouse) C:Date: 25-Mar-1993 *sequence_revision 18-Nov-1994 *text_change 05-Nov-1999 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A:Reference number: A45283; MUID:92262522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Specific antiviral activities of A; Reference number: S27387; MUID:93076908 A; Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-240-675-1_COPY_27_229 x S27387
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Quality:
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A;Residues: 1-421,'V',423-560 <LIM>
                                        A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-590 <UZE>
A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
R;Lutfalla, G; Uze, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
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A; Residues: 1-560 <MOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:A45283
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
: Uze,
1994
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3.800
84.615
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Gaps: 2
Percent Identity: 69.231
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                                                                        PID: g194112
NCBIP: 102357)
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A; Molecule type:
A; Residues: 118-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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C;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 473-590
A; Cross-references:
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A; Residues: 426-445 < RE6>
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A;Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I48425
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A; Residues: 127-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Reference number: I48423; MUID:95047447
seq_documentation_block:
hypothetical protein F23K16.
                                                              seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: IFNAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 265-375 <RE4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Percent Similarity:
                                                                                                                                            154
                                                                                                                                                                                                                          104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
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                                                                                                                                                                                                                                                                                                            54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                             ATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCC
                                                                                                                                                                                     AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                                                        MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                   HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg
                                                              pir2:T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                        to: A45283
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EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <RE7>
EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
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3.536
86.154
    40
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Gaps:
Percent Identity:
  Arabidopsis thaliana
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55.385
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try3 protein - rat

C;Species: Rattus norvegicus (Norway rat)
C;Species: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C;Accession: JC5807
C;Accession: JC5807
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T09357
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16652
A;Accession: T09357
                                                                                                                                                                                                           A;Experimental source: brain C;Comment: This protein participates in store-operated Ca2+ entry into cells. C;Superfamily: TRPC3 protein
                                                                                                                                                                                                                                                                                                                                                                             A;Title: Expression and characterization of a trpl homolog from rat. A;Reference number: JC5807; MUID:98042538
A;Accession: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JC5807
R;Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.
Biochem. Blophys. Res. Commun. 240; 167-172, 1997
Biochem. Blophys. Res. Commun. 240; 167-172, 1997
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A;Residues: 1-304 <BEV>
A;Residues: 1-304 <BEV>
A;Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.40
A;Experimental source: cultivar Columbia; BAC clone F23K16
C;Genetics:
                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-828 < PRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_229 x T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
A; Introns: 129/2; 243/2
alignment_block:
                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: ATSP: F23K16.40
                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: T09357 from: 1 to: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 lnLysVal 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 ThrArgArgLysValArgGluProArgPheCysPheLysThrLeuSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 nThrAlaSerLeuGlyValValSerSerLeuLysMetLysLys LeuLys 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 AsnGlyArgHisHisHisHisAspThrProSerArgHisAspLysHisAs 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 TCTCCTCAAAAAGTA.....GA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTCTGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uValAspValLeuAspAspGlyTyr....ArgTrpArgLysTyrGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAA 93
                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.00
1.775
57.143
                                                     71.00
1.614
60.274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 4
Percent Identity: 32.857
                              Percent Identity: 34.247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y105C5B.o - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CESP:Y105C5B.o
A;Introns: 13/1; 56/3; 155/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-194 <WIL>
A;Cross-references: EMBL:AL110479; NID:e1542153; PIDN:CAB54363.1; CESP:Y105C5B.o
A;Experimental source: clone Y105C5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, September 1999
A;Reference number: Z20208
A;Accession: T26391
                         seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_229 x T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: T26391 from: 1 to: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-1_COPY_27_229 x JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 l...IleAspTyrProLys 409
                                                                                                            160 GAGTCTGTCGGGAATGTG 177
                                                                                                                                                                                                                                          110 AGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 AsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIleThrVa 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 etLysPheValAlaAlaSerPheIleIlePheLeuGlyLeuLeuValPhe 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 rTrpIleAlaProCysSerArgLeuGlyLysIleLeuArgSerProPheM 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 LeuValValLeuValValAlaLeuAlaLeuProPheLeuAlaIleGlyTy 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 TTCATTCGATTATCAAAAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ..CAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 147
                                                                                48
                                                                                                                                                                                        \omega
                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GTCCTCCTGGGCCGACGACCCTAGTGCTCGTCGCCCGTGGGCCCATGGGT :::|||||||
                                                                                                                                                                                                                                                                                                                                                    60 GTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCT.... 99
                                                                                                                                                                                                                                                                                                                                                                                                      1 MetLeuLeuArgAlaIleLeuLeuIlePheIleSer...AlaProTrpVa 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                GluGlnValAlaAsnMet 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAGGAGCGATGAGTCTGTCGGG......AATGTGACTTT 182
                                                                                                                                                                                        isIleAsnLeuLeu.....AsnGlyIleArgGlnLysAsnAlaIleAsp
                                                                                                                                                                                                                                                                                            lLeuSerValThrValLysArgAsnMetThrGluTyrGluGlnLysIleH
                         Pir2:JQ0405
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1.756
69.643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
2
32.143
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seq_documentation_block:
hypothetical 119.5k protein
N;Alternate names: ORF 1 protein
C;Species: Micrococcus luteus, Micrococcus lysodeikticus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
C;Accession: J00405
R;Shiota, S; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A;Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: iden
A;Reference number: S04781; MUID:89364717
A;Accession: J00405
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A;Residues: 1-1106 <SHI>
A;Cross-references: EMBL:X15867
A;Note: all the codons between two in-frame stop codons are translated; the translation:
A;Note: the gene encoding this protein overlaps uvrA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S42718; S37477
R;McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.
Biochim. Biophys. Acta 1217, 219-223, 1994
A;Title: Sequence analysis of a cDNA encoding a human nuclear
A;Reference number: S42718; MUID:94154002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1475 < MCM>
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                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S42718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:S42718
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:225535; NID:g406224; PIDN:CAA80982.1; PID:g406225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: JQ0405 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                               Align seg 1/1 to: S42718 from: 1 to: 1475
                                                                                                                                       US-09-240-675-1_COPY_27_229/rev x S42718
                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Homo sapiens (man);Date: 13-Jan-1995 #text_change 05-Nov-1999;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 TCATCTATGATGTCGACCTCTACTTTTTGAGGAGATTTTAGATTTTTTCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TCACATTCCCGACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 SerProThrGlyGluThrProValSerCysPro...... 46
                             ACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTGTCATCTATGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCA 5
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Quality:
Ratio:
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2.233
46.154
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2.167
58.824
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                                                                                                                                                                                                                             Percent Identity:
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Escherichia coli uvrA gene: identification
                                                                                                                                                                                                                             39.216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex protein,
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A;ACCESSION. ...
A;Molecule type: DNA
A;Residues: 1-571 GBEV>
A;Cross-references: EMBL:AL078465; GSPDB:GN00062; ATSP:T15N24.90
A;Cross-references: cultivar Columbia; BAC clone T15N24
                                                                                                        seq_documentation_block:
    comC-alpha protein - phage T4
    N;Alternate names: gp comC alpha
    C;Species: phage T4
    A;Note: host Escherichia coli
    C;Date: 03-May-1994 *sequence_revision 03-May-1994 *text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, submitted to the Protein Sequence Database, May 1999
A;Reference number: 216518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T15N24.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T08930
                          C:Accession: A45731
R:Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4
A; Introns: 76/3; 90/3; 142/3; 311/1; 363/2; 415/2
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                                                                                                                                                                                                                                                                                                              seq_name: pir2:A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
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A; Title: Sequence and characterization of the bacteriophage T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: T08930 from: 1 to: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-240-675-1_COPY_27_229 x T08930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Gene: ATSP:T15N24.90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1248 ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThrSe 1264
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                                                                                                                                                                                                                                                                                                                                                                                                                            147 GAACAGGAGCGATGAGTCTGTC.....GGGAAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 ProAspAspAspAspProPheSerLysArgArgArgMetGluGlyAlaMe 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 tGluIleThrProLeuValLysProIleArgGluProArgValValValG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CGGACAACACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erAsnAsnThrThrSerGlyPheGlyPheGlyAlaThrThrThrSer 1297
                                                                                                                                                                                                                                                                                                                                                                       pargLysTyrGlyGlnLysValValargGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lnThrLeuSer.GluValAspIleLeuAspAspGlyTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....GTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.00
1.750
58.065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CATGGGCCCACGGCGACGAGC 36
                                                                                                                                                                                                                                                                                                                                                                             411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 62
: 4
: 33.871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
comCalpha gene produc
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A:Reference number: A45731; MUID:93015705 .
A;Accession: A45731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <SAN>
A;Cession: CB:M89919; NID:g215829; PIDN:AAA32485.1; PID:g215832
C;GenetLos:
A;Gene: comC alpha
A;Gene: comC alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: 154418
R;Sood, A.K.; Pan, J.; Biro, P.A.; Pereira, D.; Srivastava, R.; Reddy, V.B.; Immunogenetics 22, 101-121, 1985
A;Title: Structure and polymorphism of class I MHC antigen mRNA.
A;Reference number: 154418; MUID:85287366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 5.848-6.274
C;Superfamily: phage T4 comC-alpha protein
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_229 x I54418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M16102; NID:g187693; PIDN:AAA59622.1; PID:g307217 C;Superfamily: class I histocompatibility antigen; immunoglobulin homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-361 <SOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sepiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I54418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:154418
                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_27_229 x A45731
                                                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCT 165
       94
                                                 16
                                                                                        54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 sArgCysAlaGlyGly.....A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 CGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 CTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTC
                                              oTrpLeuThrGluThrTrpAlaGlySerHisSerMetArgTyrPheTyrT 33
                                                                                                                                                                                         ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splieLeuAspGiuAsnPhelle....TrpLeuSerThrAsnGluAla
                                                                                                                                            MetLeuValMetAlaProArgThrValLeuLeuLeuLeuSer...GlyPr 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histocompatibility antigen HLA-B7 alpha chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                        to: I54418 from: 1 to: 361
                                                                                                                                                                                                                                                                                                                                                       62.50
1.645
62.295
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2.155
58.000
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                                                                                                                                                                                                                                                                                                                                      Length: 61
Gaps: 2
Percent Identity: 24.590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fercent Identity: 34.000
  TCTCCTCAAAAAGTAGAGGTCGAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
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                                                                                             93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duceman, B
A;Cross-references: EMBL;U08988; NID:g571295; PID:g571296
C;Genetics:
A;Gene: GDB:CRFB4; CRF2-4
                                                                                                                                       submitted to the EMBL Data A; Reference number: G06935 A; Accession: G01418
                                                                                                                                                                                                                                     cytokine receptor family II,
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence
C;Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-240-675-1_COPY_27_229 x A26391
                                                                       A; Molecule type: DNA
A; Residues: 1-273 <LUT>
                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                             C;Accession: G
R;Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: lecithinase C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phospholipase C (EC 3.1.4.3) – Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: p1r2:A26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: A26391 from: 1 to: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 TTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 ATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 TyrValAspAspThrGlnPheValArgPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ű
                                                                                                                                                                                                                                                                                                                                                                                                                          pPheGln 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTGAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                          family II, member 4 - human
                                                                                                                                                                                                                                                            #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.00
1.824
49.275
                                                                                                                                                                                    Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity:
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C;Species: Pseudomonas aeruginosa
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 08-Oct-1999
C;Accession: A26391
R;Pritchard, A.E.; Vasil, M.L.
J. Bacteriol. 167, 291-298, 1986
A;Title: Nucleotide sequence and expression of a phosphate-regulated gene encoding A;Reference number: A26391; MUID:86250607
A;Accession: A26391
A;Recession: A26391
A;Recession: A26391
A;Residues: 1-730 <PRI>
A;Cross-references: GB:M13047; NID:g151492; PIDN:AAA25966.1; PID:g151493 C;Keywords: phosphoric diester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hrSerValSerArgPro******GlyGluProArgPheIleSerValGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipophosphodiesterase
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytokine receptor family class II protein CRF2-4 precursor - human C;Species: Homo sapiens (man) C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997 C;Accession: A47003 R;Lutfalla, G; Gardiner, K.; Uze, G. Genomics 16, 366-373, 1993 R;Title: A new member: A47003; MUID:93300510 A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-240-675-1_COPY_27_229 x G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Map position: 21q
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_27_229 x A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:Z17227; NID:g393378; PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: G01418 from: 1 to: 273
                                                                                                                                                                                                                                                                                          Align seg 1/1 to: A47003 from: 1 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                         134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TCATTCGATTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCT.....
                                                                                                                                                                                                                        55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCT.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
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                                                                                              19 yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                         3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                              .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.50
1.922
59.259
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1.922
59.259
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Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 29.630
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52
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Le, T.; Waterston, R.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid F08D12.
A;Reference number: Z20068
A;Accession: T25677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
hypothetical protein F08D12.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_229 x T25677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-340 <LETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:F08D12.9
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U80840; PIDN:AAB37931.1; GSPDB:GN00020; CESP:F08D12.9
A;Experimental source: strain Bristol N2; clone F08D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 28/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T25677
                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: T25677 from: 1 to: 340
                                                      188 TCGATTATCAAAAA 201
                                                                                                                                                                138 CCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 TCATTCGATTAT 195
98 alGlyTyrGlnGln 102
                                                                                                         82 p...ArgTrpAsnLeuAsnPheCysGluIleAlaAsnValThrTyrThrV 98
                                                                                                                                                                                                                      66 LeuThrAsnGlnGluGluIleArgLeuAspValLysThrAspArgPheAs 82
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Gaps: 1
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Swissprot_38:IRSZ_MOUSE -
Swissprot_38:SFR2_CHICK +
Swissprot_38:SFR2_CHICK +
Swissprot_38:SFR2_HUMAN +
Swissprot_38:SFR2_HUMAN +
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Swissprot_38:FR2_BACSU +
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Swissprot_38:SFR3_HUMAN +
Swissprot_38:FR2_ECOLI -
Swissprot_38:GTR1_RAT +
Swissprot_38:SFR3_HUMAN -
Swissprot_38:SFR3_HUMAN -
Swissprot_38:GTR1_CAUPO -
Swissprot_38:GUNZ_CLOSR +
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Swissprot_38:MOVP_TMVTO -
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Swissprot_38:INR1_BOVIN
Swissprot_38.Tun.
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SwissProt_38:N153_HUMAN
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-Q-/cgn2_1/USPTQ.spool/US09240675/runat_30052000_164313_24686/app_query.fasta.1
-Q-/cgn2_1/USPTQ.spool/US09240675/runat_30052000_164313_24686/app_query.fasta.1
-DB-Sw1ssProt_38 -QFMT-fastan -SUFFIX-modif.rsp -GAPOP=12.000
-GAPDXT-4.000 -MIMMATCH-0.100 -LOOPCL-0.000 -LOOPCXT-0.000
-QGAPDXT-4.000 -QGAPEXT-0.050 -XGAPEXT-0.500
-TGAPDP-4.500 -QGAPEXT-7.000 -YGAPOP=10.000 -XGAPEXT-0.500
-TGAPDP-6.000 -FGAPEXT-7.000 -YGAPOP=10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -NTRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCt
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NC_XLPXY -WAIT
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| Documentation | 557 | P17181 | hom | 558 | p17181 | hom | 560 | Q04790 | p3896 | mu | 1475 | p49790 | p3896 | mu | 1475 | p49790 | p3896 | mu | 1475 | p49790 | p3896 | mu | p3896 | mu | p3896 | p3996 | p3
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3 1.4e-34
2 3.4e-18
10 1.4e-17
                                                                                        pl 11167 rattus norvegicus (rat)
print of the control of the contr
                                                                                                                                                                                                                                                                                                            1 1 001330 homo sapiens (human).
5 1 p31260 homo sapiens (human).
35 1 00837 plassmodium falciparu
9 1 p72404 streptomyces coelicol
0 1 p22452 bacillus subtilis. fl
0 05736 methanococcus jannasc
1 p15893 spiroplasma virus spvl
6 1 p20599 triticum aestivum (wh
6 1 p20599 briticum aestivum (wh
6 1 p20599 braillus subtilis. pro
6 1 p20592 erwinia chrysanthemi.
1 p24417 bacillus subtilis. pro
1 p39906 klebsiella pneumoniae
1 p28719 zymomonas mobilis. dn
9 1 p39906 klebsiella pneumoniae
1 03457 bacillus subtilis. rit
1 p50766 human papillomavirus t
4 1 p27316 rift valley fever v
4 1 p23152 homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 P06200 pseudomonas aeruginos
1 Q08334 homo sapiens (human)
1 P70459 mus musculus (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p81122 mus musculus (mouse; p30352 gallus gallus (chick p27884 oryctolagus cuniculus) p28594 anabaena sp. (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q01438 bacteriophage t4. com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q04790 bos taurus (bovine).
Q28589 ovis aries (sheep).
P33896 mus musculus (mouse)
        P03584 tobacco mosaic virus P29799 tomato mosaic virus P28099 alopías vulpinus (t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapiens (human)
              SwissProt_38: VPHE_NPVAC
SwissProt_38: VIE4_FRG3V
SwissProt_38: ENV2_MOUSE
SwissProt_38: DHE4_EMENI
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        DOMAIN
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                                                                                              DOMAIN
TRANSMEM
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                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                        Receptor; Transm
Phosphorylation.
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MEDLINE; 90124632.
                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                  Transmembrane;
              28
437
458
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199
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seq_name: SwissProt_38:INR1_HUMAN
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A Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
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MEDLINE; 92129376.

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;

"The structure of the human interferon alpha/beta receptor gene.";

J. Biol. Chem. 267:2802-2809(1992).
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1917181;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J03171; AAA52730.1; -.
EMBL; X60459; CAA42992.1; -.
PIR; A32694; A32694
PIR; S17112; S17112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Uze G., Lutfalla G., Gresser I.;
Uze G., Lutfalla G., Gresser I.;
"Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";
Cell 60:225-234(1990).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
CHAIN.
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P14358
P11370
P18819
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70 mus musculus (mc
9 emericella n'a
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alignment_scores:
Quality:
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                                                                                                                                                                    seq_documentation_block:
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SEQUENCE
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CARBOHYD
MEDLINE; 13076908.

Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

"Specific antiviral activities of the human alpha interferons determined at the level of receptor (IFNAR) structure.";

FEBS Lett. 313:255-259(1992).
                                                                                                         INRI_BOVIN STANDARD; PRT; 560 AA.
004790;
01-CCT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNAR1 OR IFNAR.
                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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MEDLINE; 93305725.

Lim J.-K., Langer J.A.;

"Cloning and characterization of a boyine alpha interferon receptor.";

Biochim. Biophys. Acta 1173:314-319(1993).

-!- FUNCTION: RECEPTOR FOR INTERPERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

SUBUNITS THEMSELVES.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
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EMBL; L06320; AAA02571.1; -.
PIR; S33770; S33770.
PIR; S27387; S27387.
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            154 AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 198
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                                                snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                           AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                     gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                         MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla...
SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln
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BY SIMILARITY.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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Gaps:
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seq\_name: SwissProt\_38:INR1\_SHEEP

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documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pregnancy.";
Endocrinology 138:4757-4767(1997).
Endocrinology 138:4757-4767(1997).

-i- function: Receptor for interferons alpha and beta, binding to tri-
-i- function: Treceptor for interferon of a number of proteins
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
SUBUNITS TEMPERANCE T MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovidae;
            CARBOHYD
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CARBOHYD
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DISULFID
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TRANSMEM
                                                                                                                                                                                                                                                                                 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CONCEPTUS AT DAY 15 OF PREGUNANCY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-ENDOMETRIUM;
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Q28589; Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
"Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                       EMBL; X95939; CAA65183.1; -. EMBL; U65978; AAB84231.1; -.
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MEDLINE; 98006426.
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BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL)
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alignment_scores:
Quality:
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    INR1_MOUSE STANDARD;
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CONFLICT
CONFLICT
SEQUENCE
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WIZE G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;

"Behavior of a cloned murine interferon alpha/beta receptor expression to the state of the 
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
EMBL; M89641; AAA37890.1; -. PIR; A45283; A45283. MGD; MGI:107658; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
15-FBB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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                                                         McMorrow I., Bastos R., "Sequence analysis of a protein, hnup153.";
                                                                                                            Eukaryota;
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                                                                                MEDLINE;
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                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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PROTEIN NUP153 (NUCLEOPORIN NUP153) (153
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01-OCT-1993 (Rel. 27, L
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"Sequence and characterization of the bacteriophage gene product, a possible transcription antitermination of the bacteriophage and the sequence of the sequen
                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 93015705. Sanson B., Uzan M.;
                                                                                                                                                                                                                                                                                                            COMCA OR GOF.
Bacteriophage T4.
Viruses; dsDNA viruses,
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PHIC PSEAE STANDARD;
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PIR; A45731; A45731.
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                 -1- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO PHOSPHATIDYLCHOLINE.
-1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O - 1,2-DIACYLGLYCEROL + CHOLINE PHOSPHATE.
-1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
HEMOLYTIC PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (HEAT LABILE-
                                                                                                                                                                                        Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases -- I- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO
                                                                                                                                                                                                                                                                               Pritchard A.E., Vasil M.L.;
"Nucleotide sequence and expression of a phosphate-regulated encoding a secreted hemolysin of Pseudomonas aeruginosa.";
J. Bacteriol. 167:291-298(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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Gaps: 3
Percent Identity: 34.000
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                in no way
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seq_documentation_block:
ID CRF4_HUMAN STANDA
AC 008334;
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1995 (Rel. 31,
DT 01-CCT-1996 (Rel. 31,
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DT 01-CCT-1996 (Rel. 31,
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1996 (Rel. 31,
DT 01-FEB-1996 (Rel. 31,
RA LUTEALIA G., Gardiner
RT 7A new member of the
RT 21 at less than 35 kt
RL Genomics 16:366-373(1
RN (2)
RN SEQUENCE FROM N.A.
RY MEDLINE; 96054036.
RA LUTEALIA G., MCInnis
RT Genomics 16:36-373(1
RN (2)
RN SEQUENCE FROM N.A.
RY MEDLINE; 96054036.
RA LUTEALIA G., MCInnis
RT neighbor.";
RL J. MO1. EVOL. 41:338
CC -i-FUNCTION: IS PROJ
CC -i-SUBCELULAR LOCAN
CC -i-SUBCELLULAR LOCAN
CC -i-SUBLIARITY: BELOCH
CC -i-SUBLIARITY: CONTY
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                            SEQUENCE FROM N.A.
MEDLINE; 96054036.
Lutfalla G., McInnis M.G., Ant
"Structure of the human CRFB4
neighbor.";
                                                                                                                                                                                                                                                                                                            TISSUE-FETAL BRAIN;
MEDLINE; 93300510.

Lutfalla G., Gardiner K., Uze G.;

"A new member of the cytokine receptor
21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-007-1996 (Rel. 34, Last annotation update)
CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457
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us-09-240-675-1_COPY_27_229 x CRF4_HUMAN
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EMBL; U08988; AAA86872.1;
PIR; A47003; A47003
HSSP; P13726; 1DAN.
MIM; 123889; -
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CARBOHYD
                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
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                                                             Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                             P70459;
                                                                                                                                                                                                                                                                       ERF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
SEQUENCE FROM N.A
STRAIN-129/SVJ;
                                                                                                                                                                                                                                                                                                                                                                                      53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                      ThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
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Ratio:
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49
68
102
161
124
273
325
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1.922
59.259
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                                                      Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal "POTENTIAL.
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FLGHP -> VGRME (IN REF. 2).
MISSING (IN REF. 2).
66706C79F8514B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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Gaps:
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Sed 12 COS
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US-09-240-675-1_COPY_27_229/rev x ERF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                      documentation_block:
IRS2_MOUSE STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation.

DNA_BIND 27
DOMAIN 166
DOMAIN 290
DOMAIN 362
DOMAIN 420
DOMAIN 420
MOD_RES 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu D., Pavlopoulos E., Modi W., Moschonas N., Mavrot "ERR: genomic organization, chromosomal localization analysis of the human and mouse genes."; Oncogene 14:1445-1451(197).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN CELLULAR PROLIFERATION (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.

PHOSPHOXYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).
                                                                                                                                                                                                                 391
                                                                                                                                                                                                                                                                           375 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q01543; 1FLI.

MGD; MGI:109637; ERF.

PRINTS; PR00454; ETSLOMAIN.

PROSITE; PS00345; ETSLOMAIN_1; 1.

PROSITE; PS00346; ETSLOMAIN_2; 1.

PROSITE; PS50061; ETSLOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U58533;
EMBL; U58534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                            Mus musculus (Mouse)
                                                                                                                                                                                                                                              32 AGGGTCGTCGCGCCCAGGAGGA 11
                                                                                                                                                                                                                 aGlyGluLysAlaProGlyGly 398
                                                                                                                                                                                                                                                                                                          TTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1 ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
                                                                                                                                                                                   SwissProt_38: IRS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
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AAC09474.1;
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75.000
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                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
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POLY-GLY.
POLY-SER.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SAC1B72FB2743FE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY ERK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETS-DOMAIN.
                                                                                                                                      PRT;
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6
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Gaps:
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45.833
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 Mammalia;
Mus.
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promoter
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OC SEE DIT A LICE
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US-09-240-675-1_COPY_27_229/rev x IRS2_MOUSE
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                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                   _documentation_block:
SFR2_CHICK STANDARD;
                                                                                                                                                                                                                          1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sun X.J., Wang L.-M., Zhang Y., Yenush L., Myers M.G. Jr., Glasheen E., Lane W.S., Pierce J.H., White M.F.; "Role of IRS-2 in insulin and cytokine signalling."; Nature 377:173-177(1995).

-i- FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
SFRS2.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:109334; IRS2. RPRINTS; PR00628; INSULINRSI. PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEART AND SPLEEN.
-!- SIMILARITY: CONTAINS 1
-!- SIMILARITY: CONTAINS 1
HSSP; P35568; 11RS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 95405472.
Sun X.J., Wang L.-M., Zhang Y., Yenush L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                      48
                                                                                                                                                                                            CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA 14
                                                                                                                                                                               oThrAlaGlySerSerMet.SerSerGluProGly 1056
                                                                                                                                                                                                                                                    GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC
                                                                                                                                                     SwissProt_38:SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1303
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187
536
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449
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Gaps: 1
Percent Identity: 51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PH DOMAIN.
PTB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ASN.
POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                            POLY-SER.
W; 5069CE9D614960C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY INSR) (BY SIMILARITY).
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                                                                                                                    PRT;
                                                                                                                    221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUNG, BRAIN, LIVER, KIDNEY
                                                         FACTOR SC35) (SC-35)
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seq_documentation_block:
ID CCAA_RABIT STAN
AC P27884: P27883.
                                                                    seq_name: SwissProt_38:CCAA_RABIT
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US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vellard M., Sureau A., Soret J., Martinerie C., Perbal B.;
"A potential splicing factor is encoded by the opposite strand of the trans-spliced c-myb exon.";
Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
-!- FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND INTERACTS WITH SPLICEOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3' SPLICE SITES DURING SPLICEOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPS WITH PRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X62446; CAA44306.1; -. PIR; S17327; S17327. PIR; B42701; B42701. HSSP; P19339; ISXL.
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                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00030; RNP_1; PFAM; PF00076; xrm; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
                                                                                                                                                                                                                44 CCGTGGGCCCATGGGTGTTGTCCGC.....AGCCGCAGGTGGA
                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY PRODUCED BY ALTERNATIVE SPLICING.
PRODUCED BY ALTERNATIVE SPLICING.
PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE DOMAIN (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                 GGTCGTCCTCCT......GGGCGCGACGACCCTAGTGCTCGTCG
                                                                                                                                          AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGA 116
                                                                                                                                                                                                                                                  GlyArgProProAspSerHisHisSerArgArgGlyProProProArgAr
                                                                                                       rgArgSerArgSerArgSerArgSerArg
                                                                                                                                                                             gTyrGlySerSerGlyTyrGlyArgArgSerArgSerProArgArgArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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111
117
221 AA;
                  STANDARD;
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62
116
221
25524 .
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2.500
53.333
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Gaps:
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                                                                                                                                                                                                                                                                                                                        from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-BINDING (RNP2) (BY SIMILARITY).
RNA-BINDING (RNP1) (BY SIMILARITY).
GLY-RICH (HINGE REGION).
ARG/SER-RICH (RS DOMAIN).
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75A4D8FF9170F1BF CRC64;
                    2424 AA
                                                                                                           137
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RI CYCDIASMIC CHINGET OF THE ALPHA 1 SUDDUILT. F.

RI NACUTE 368:67-70(1994).

RI CYCDIASMIC LINKET OF THE ALCIUM CHANNELS (VSCC) MEDIATE THE CC. IN CYTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE CC. IN A VARIETY OF CALCIUM INTO EXCLIDANCE CELLS AND ARE ALSO INVOLVED CC. IN A VARIETY OF CALCIUM CERVENTENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CC. CHANNELS BELONG TO PAND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM CC. CHANNELS BELONG THE FIGH-VOLTAGE ACTIVATED" (HVA), GROUP AND CC. IVA (OMEGA-ACA-IVA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-ACA-IVA). THEY ARE HOWEVER INSENSITIVE TO COMPLEXES, CONSISTING OF ALPHA-1, SUBJUNIT. IN MANY CASES, THIS CONCELLENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, SUBJUNITS. IN MANY CASES, THIS CHANNEL ACTIVITY. THE AUXILIARY SUBJUNITS BETA AND DELTA SUBJUNITS. CC. IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBJUNITS. IN MANY CASES, THIS CC. IN A 1:1:1:1 RATIO. THE AUXILIARY SUBJUNITS BETA AND ALPHA-2/DELTA CLANNEL ACTIVITY. THE AUXILIARY SUBJUNITS BETA AND ALPHA-2/DELTA CC. INSURED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC. IN A 1:1:1:1 RATIO. THE GANIN HERED, ASPONDUCED BY ALTERNATIVE CC. IN THE BRAIN, A SHORT ISOFORM BI-1/1A-1 AND ALDELTA SUBJUNITS. BETA AND ALPHA-2/DELTA CC. INTEGRAL MEXERANCE PACTOLIUM.

CC. INTURBATION OF THE FORM HERED, ARE PRODUCED BY ALTERNATIVE CC. THE Q-TYPE BEING A PROMINENT CALCIUM CC. INTEGRAL MEXERANCE PACTOLIUM.

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MEDIA-SUBUNIT BINDING DOMAIN, AND MEDILNE; 94150724.
Pragnell M., de Waard M., Mori Y Campbell K.P.;
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Cantolum channel beta-subunit b/
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15-FEB-2000 (Rel.
VOLTAGE-DEPENDENT I
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EMBL; X57477; (EMBL; X57689; (EMBL; X57476; EMBL; X57476; EMBL; X57688; (EMBL; X57688; (EMBL); X57688; (EMBL);
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MORI Y., Friedrich T., Kim M:-S., Mikami A.,
BOSSE E., Hofmann F., Flockerzi V., Furuichi
Imoto K., Tanabe T., Numa S.;
"Primary structure and functional expression
of a brain calcium channel.";
Nature 350:398-402(1991).
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Oryctolagus cuniculus (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                   modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch)
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CAA40715.1;
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. 26, Last sequence update)
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ALPHA-1 POLYPEPTIDE ISOFORM
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T., Mikoshiba F
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Calcium channel; Glycoprotein; Repeat; Multigene family;
Calcium-binding; Phosphorylation; Alternative splicing.
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01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
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SEQUENCE FROM N.A. MEDLINE; 92268848. Linear J.R.; Fundamental J.R.; Fundamental J.R.; Fundamental J.R.; Fundamentification, characterization and sequence analysis of the gene "Identification, characterization and sequence analysis of the gene encoding phosphoenolpyruvate carboxylase in Anabaena sp. PCC 7120.";
                                                                              Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
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MISSING (IN ISOFORM BI-1/1A-1).
MISSING (IN ISOFORM CBS).
MISSING (IN ISOFORM CBS).
A -> T (IN ISOFORM CBS).
S -> N (IN ISOFORM CBS).
E->S: REDUCED BETA-SUBUNIT INTERACTION.
L->H: REDUCED BETA-SUBUNIT INTERACTION.
Y->S: REDUCED BETA-SUBUNIT INTERACTION.
Y->S: REDUCED BETA-SUBUNIT INTERACTION.
Y->S: REDUCED BETA-SUBUNIT INTERACTION.
Y->S: REDUCED BETA-SUBUNIT INTERACTION.
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CALCIUM ION SELECTIVITY AND PERMEABILITY
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PIR; A44831; A44831.

PROSITE; PS00150; PEPCARBXLASE.

PROSITE; PS00153; PEPCASE_2; 1.

PROSITE; PS00781; PEPCASE_1; 1.

PRAM; PF00311; PEPCASE; 3.

Lyase; Carbon dioxide fixation; Al

Tricarboxylic acid cycle.

ACT_SITE 52 525

ACT_SITE 52 628 82 SEQUENCE 982 AA; 112679 MW; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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                                                 SEQUENCE FROM N.A., AND MEDLINE; 92237694. Fu X.-D., Maniatis T.;
                                                                                     SFROE.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Hominidae; Homo.
                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
splicing factor, Arginine/Serine-Rich 2 (Splicing Factor Sc35) (SC-35)
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SEQUENCE FROM N.A.

Perbal B.;

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Sureau A., Perbal B.;
Sureau A., Perbal B.;
Several mRNAs with variable 3' untranslated regions and different
"Several mRNAs with variable 3' untranslated regions and different
stability encode the human PR264/SC35 splicing factor.";
Proc. Natl. Acad. Sci. U.S.A. 91:932-936(1994).
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MEDINE: 92212859.

Vellard M., Sureau A., Soret J., Martinerie C., Perbal B

"A potential splicing factor is encoded by the opposite

trans-spliced c-myb exon.";

Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
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"The PR264/c-myb connection: expression of a splicing factor
modulated by a nuclear protooncogene.";
Proc. Natl. Acad. Sci. U.S.A. 89:11683-11687(1992).
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MEDLINE; 95354672.

Tacke R., Manley J.L.;

"The human splicing factors ASF/SF2 and SC35 possess distinct, functionally significant RNA binding specificities.";

EMBO J. 14:3540-3551(1995).
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"Protein-protein interactions and 5'-splice-site recognity."
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Nature 368:119-124(1994).
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                                                                                                                                                                                                                                FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND INTERACTS WITH SPLICEOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3' SPLICE SITES DURING SPLICEOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPS WITH PRE-MRNA. INTERACTS WITH OTHER SPLICEOSOMAL COMPONENTS, VIA THE RS DOMAINS, TO FORM A BRIDGE BETWEEN THE 5' AND 3' SPLICE SITE BINDING COMPONENTS, U1 SNRNP AND U2AF. IN VITRO, BINDS SF2/ASF, U1-70K AND THE 35 KD BUT NOT THE 65 KD SUBUNIT OF U2AF. BINDS TO PURINE-RICH RNA SEQUENCES, EITHER 5'-AGSAGAGTA-3' CAN BIND TO BETA-GLOBIN MRNA AND COMMIT IT TO THE 5' COTTCGAGTA-3'. CAN BIND TO BETA-GLOBIN MRNA AND COMMIT IT TO THE SPLICENCE PATHWAY.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY BE PRODUCED BY ALTERNATIVE SPLICING.
PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RESTRICT OF THE PROPERTY OF THE PROPERT
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seq_documentation_block:
ID HXAA_HMMAN STANDA
AC P31260; Q15949;
DT 01-JUL-1993 (Rel. 26,
DT 15-FEB-2000 (Rel. 39,
DE HOMEOBOX PROTEIN HOX-
GN HOXA10 OR HOX1H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; C
CC Eutheria; Primates; C
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91288229.
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US-09-240-675-1_COPY_27_229 x SFR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_38:HXAA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M90104; AAA60306.1; -. EMBL; X62447; CAA44307.1; -. EMBL; X75755; CAA53383.1; -. EMBL; L03693; AAA60162.1; -. PIR; S17328; S17328. PIR; A42634; A42634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation.
DOMAIN 16
DOMAIN 55
DOMAIN 111
DOMAIN 117
CONFLICT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  P31260; Q15949;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
HOMEDBOX PROTEIN HOX-Al0 (HOX-1H) (HOX-1.8) (PL)
                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                          143
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                                                                                                                                                                                                                                                                                                                                                           126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 GlyArgProProAspSerHisHisSerArgArgGlyProProProArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP). SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                          ArgTyrSerArg 146
                                                                                                                                                                                                                                                                                                                          CGACATCATAGA
                                                                                                                                                                                                                                                                                                                                                         rgArgSerArgSerArgSerArgSerArgSerArgSerArgSer 142
                                                                                                                                                                                                                                                                                                                                                                                           TCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                            gTyrGlyGlyGlyTyrGlyArgArgSerArgSerProArgArgArgA 126
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6
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116
221
                                                    Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
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Percent Identity:
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RNA-BINDING (RNP1) (BY SIMILARITY).
GLY-RICH (HINGE REGION).
ARG/SER-RICH (RS DOMAIN).
R -> G (IN REF. 2 AND 3).
                                                                                                                                                                                                         PRT;
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2
35.185
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sp_invertebrate:021784 +
sp_invertebrate:016867 +
sp_invertebrate:021494
sp_fungi:008912 +
sp_rodent:088277 +
5
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sp_rodent:Q62143 +
sp_mhc:Q30849 +
sp_fung1:Q9Y775 +
sp_plant:Q08700 +
sp_lant:Q08700 +
sp_invertebrate:Q18109 +
sp_invertebrate:Q25994 +
sp_bacteria:Q86774 -
                                                                                                                                                                                                                             sp_plant:09xID0
sp_plant:023740
sp_plant:09xFW5
sp_plant:012866
sp_plant:065711
sp_virus:065450
  sp_virus:Q81166
sp_invertebrate:(
sp_lant:023854
sp_plant:064680
sp_human:075167
o_plant:023292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mamma1:077699
sp_human:095927
sp_rodent:088970
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Query: US-09-240-675-1_COPY_27_229
Query length: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 225878
Database length: 69334122
Search time (sec): 89.94001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent:060805
sp_human:09Y5L9
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sp_invertebrate:023047
sp_redent_cross
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sp_plant:O64410
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sp_human:Q13507 +
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                                                                                                                                                                                                                                                                                                                                                       sp_bacteria:Q9X4V6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_human:Q9Y4L5
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-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24664/app_query.fasta.1
-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24664/app_query.fasta.1
-DB-SPTREMBL_12 -QFMT-fastan -SUFFIX-modif.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINANCH=0.100 -LOOPCLE-0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=7.050 -XGAPOP=10.000 -XGAPEXT=0.500
-TGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START1 - AMTRIX-blosum62
-TRANS-human40.cd1 -LIST=45 -DCCALICN=200 -THR_SCORE-pct
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAXILEN=1000000 -USER-US09240675 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results were Copyright (c)
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) 1993-2000 Compugen Ltd.
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+ 60.50 124.46 23.91

+ 60.00 122.21 27.40

+ 60.00 122.21 27.40

+ 60.00 112.66 23.37

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59.50 127.79 33.49

59.50 123.89 32.43

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    18 (01307 homo sapiens (human). tr

17 (07769) bos taurus (bovine). tr

19 (095927 homo sapiens (human). dr

19 (08970 mus musculus (mouse). ir

10 (08970 mus musculus (human). hy

10 (19415 homo sapiens (human). hy

10 (19412) caenorhabditis elegans

10 (19410 zea mays (maize). cytoch

10 (19424 caenorhabditis elegans

10 (19424 caenorhabditis elegans

10 (19424 caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! Documentation
                                                                                                                                                            Q9yeb6 aeropyrum pernix. 108aa | Q052143 mus musculus (mouse). q8 | Q30849 oryctolagus cuniculus (yeas | Q05714 streptcalis (yeas | Q08700 brassica napus (rape). s | Q9yfw6 brassica oleracea (cauli oleracea) | Q25994 plasmodium falciparum | Q80774 streptcmyces granaticolor | Q9yfw6 brassica oleracea (cauli oleracea) | Q12866 homo sapiens (human). ce | Q65711 arabidopsis thaliana (mc) | Q65450 pestivirus type 3. nonsti oleracea | Q1494 caenorhabditis elegans | Q14
1 008912 saccharomyces cerevisiae 1 088277 rattus norvegicus (rat) 1 081166 hepatitis b virus. core 1 09xyt5 cassiopea xamachana. s 1 023854 brassica campestris (fie 1 054860 arabidopsis thaliana (md 1 075167 homo sapiens (human), ki 1 023292 arabidopsis thaliana (md
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9yhw0 gallus gallus (chicken)
1 Q9y5t6 homo sapiens (human)
1 Q76514 caenorhabditis elegan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q60805 mus musculus (mouse). c: Q9y519 homo sapiens (human). t
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sp_bacteria:034557 +
sp_plant:Q38704 +
sp_plant:Q39363 +
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                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                  seq_name: sp_human:Q9Y5T6
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SEQUENCE
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    TISSUE-TESTIS;
MEDLINE; 98288806
                                                                                                                                                                                                                                                                          Q9Y5T6
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                                             SEQUENCE FROM N.A.
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alignment_block:
US-09-240-675-1_COPY_27_229 x Q9YHW0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q9YHW0 from: 1 to:
BRX.

BRX.

Homo sapiens (Human),

Homo sapiens (Human),

""'Paryota; Metazoa; Chordata; Cr
"""Attes; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus (Ghicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                  01-NOV-1999 (TIEMBLIE1. 12, Created)
01-NOV-1999 (TIEMBLIE1. 12, Last sequence update)
01-NOV-1999 (TIEMBLIE1. 12, Last annotation update)
BREAST CANCER NUCLEAR RECEPTOR-BINDING AUXILIARY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TREMBLrel. 10, Creat. 01-MAY-1999 (TREMBLrel. 10, Last. 01-MAY-1999 (TREMBLrel. 10, Last. INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative genomic analysis receptor gene cluster."; Genome Res. 0:0-0(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF082664; AAD13669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REBOUL J., GARDINER K.,
                                                                                                                                                                                                                                                                                                                                                                                   GGGAATGTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                   laValAsnThrAsnPheThrLeuMetTrpAsnTyrThrGlyAspGlyThr
                                                                                                                                                                                                                                                                                                                                                    TCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyArgLeuAlaAlaVa,LLeuLeuCysValLeuValValValSerArgCy
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                                Craniata;
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interferon/interleukin-10
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                                  Vertebrata;
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034557 bacillus subtilis.
038704 avena fatua. dna-b
039363 brassica napus (ra
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seq_documentation_block:
ID 076514;
AC 076514;
AC 076514;
DT 01-NOV-1998 (TIEMBLIE
DT 01-NOV-1998 (TIEMBLIE
DT 01-NOV-1999 (TIEMBLIE
DT 01-NOV-1998 (TIEMBLIE
DT 1987)
DT 1987; P18075; 1BMP-
DR PINITS; PR00438; GFCY
SEQUENCE 365 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_27_229 x Q9Y5T6
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: sp_invertebrate:076514
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1274 GlnLysGlnLeuGluArgGluGlnGluHis...ValArgArgGluAlaG1 1289
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MORITA K., CHOW K.L., UENO N.;
"Body Length and Male Tail Ray Pattern Formation of C. elegans
"Budy Length and Male Tail Ray Pattern Formation of C. elegans
"Budy Length and Male Tail Ray Pattern Formation of C. elegans
"Budy Length and Male Tail Parily.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF074395; AAC26791.1;
HSSP; P18075; 1BMP.
PFAM; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
SEQUENCE 365 AA; 41781 MW; 54051BEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUBINO D., DRIGGERS P., ARBIT D., KEMP L., MILLER B., COSO O., PAGLIAI K., GRAY K., GUTKIND S., SECARS J.;

"Characterization of Brx, a novel Dbl family member that modul estrogen receptor action.";

Oncogene 16:2513-2526(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysSe 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....TATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1429 AA; 161033 MW;
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Last sequence update)
Last annotation update)
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 1429
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Gaps: 5
Identity: 41.892
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alignment\_scores:

351 LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGlyTy 367

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Seq_documentation_block:
ID 013507; 000593;
DT 01-NOV-1996 (TYEMBLEE DT 01-NOV-1996 (TYEMBLEE DT 01-NOV-1996 (TYEMBLEE DT 01-NOV-1999 (TYEMBLEE DT 01-NOV-1999 (TYEMBLEE DT 01-NOV-1999 (TYEMBLEE DT 01-NOV-1999 (TYEMBLEE DE TRANSIENT RECEPTOR PG GN TRPC3 OR HTRP3.
OC EURATYOCE; Metazoa; C EURATYOCE; Metazoa; C EURATYOCE; Metazoa; C C EURATYOCE; Metazoa; C C EURATYOCE; Metazoa; C C C EURATYOCE; Metazoa; Meta
                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_229 x Q13507
                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
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US-09-240-675-1_COPY_27_229 x 076514
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                                                                 Align seg 1/1
                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97358541.

XU X.Z.S., LI H.S., GUGGINO W.B., MONTELL C.;

"Coassembly of TRP and TRPL produces a distinct sto
conductance.";

Cell 89:1155-1164(1997).

EMBL; W47050, AACS1653.1; -.

EMBL; Y13758; CAA74083.1; -.

EMBL; Y13758; CAA74083.1; -.

PFAM; PF00022; ank; 2.

PFAM; PF00079; TRNSRECEPTRP.

SEQUENCE 848 AA; 97354 MW; 78AC2E9D CRC32;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     013507; 000593;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
TRPC3 OR HTRP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "trp, a novel mammalian gene capacitative Ca2+ entry."; Cell 85:661-671(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 96234226.
ZHU X., JIANG M., PEYTON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
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:::||||||::: |||||||
4 ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT 126
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                                                                 Q13507
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54.667
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1.941
62.963
                                                                 from: 1
                                                                                                                                                                                                                        Percent Identity:
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seq_name: sp_human:095927
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Quality:
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Percent Similarity:
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077699 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
WISSENBACH U., PHILIPP S., FLOCKERZI V.;
WISSENBACH U., PHILIPP S., FLOCKERZI V.;
"Cloning and analysis of TRP channels.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ006781; CAA07246.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRP3 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AGGTGGAACAGGAGCGATGAGTCTGTCGGG......AATGT 176
                                                                                                                                                                                                                                                                             104 AAGTAGAGGTC......GACATCATAGATGACAACTTTATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                91
                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                        41 rTrpIleAlaProCysSerArgLeuGlyLysValLeuArgSerProPheM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eThrValThr...AspTyrProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTAGAGGTC.....GACATCATAGATGACAACTTTATCCTG
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                                                                                         GACTTTTTCATTCGATTATCAAAAA 201
                                                                                                                                       ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl
                                                                                                                                                                                   AGGTGGAACAGGAGCGATGAGTCTGTCGGG.......AATGT 176
                                                                                                                                                                                                                                   etLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeuLeu 74
                                                                                                                                                                                                                                                                                                                                                                         ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
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LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGlyTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGTCGTCCTGGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
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                                              eThrVal...IleAspTyrProLys 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 077699
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1.512
54.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 75
Gaps: 3
Percent Identity: 33.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B9F9B808 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400
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seq_documentation_block:
ID 088970;
AC 088970;
DT 01-NOV-1998 (TrEMBLrel 08
DE INSULIN RECEPTOR SUBSTRATE
GN IRS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chorda:
OC Eukaryota; Metazoa; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID 095927
AC 095927
PRELIMINA
AC 095927
DT 01-MAY 1999 (TrEMBLre
DT 01-MAY 1999 (TREMBLre
DT 01-MAY 1999 (TREMBLRe
DT 01-MAY 1999 (TREMBLRe
DE DJ465N24.2.1 (PUTATIV
GN DJ465N24.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; C
C Eutheria; Primates; C
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON S.;
RA SUBMITCHE (FEB-1999)
DR EMBL; AL031432; CAB37
SQ SEQUENCE 290 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allgnment_block:
US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: sp_rodent:088970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: 095927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                             SEQUENCE FROM N.A.
XU G., ULMER W.T., WOLF B.A.;
"Partial genomic DNA sequence of mouse beta-cell IRS-2.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090738; AAC61743.1; -.
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; ALO31432; CAB37992.1; -. SEQUENCE 290 AA; 33613 MW; B59EOC18 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update
DJ465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
DJ465N24.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INSULIN RECEPTOR SUBSTRATE-2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Homo sapiens (Human).
Finkarvota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 AAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 rgSerHisSerArgValSerSerArgPheSerSerArgSerArgArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 GlySerProGlnGluLysAspSerProSerThrSerArgSerGlyGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AGGTGGAAAAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysSerArgSerArgSerArgArgArgHisGlnArg
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2.296
43.548
               75251 MW;
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Gaps:
Percent Identity:
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               B3410CAF CRC32;
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1
29.032
                                                                                                                                                                                                                                                                                                         Mammalia;
Mus.
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alignment\_scores: Quality: Ratio: Percent Similarity:

61.00 2.652 79.310

Length: Gaps: Percent Identity:

29 1 51.724

alignment\_block: US-09-240-675-1

\_COPY\_27\_229/rev x 088970

Align seg 1/1 to: 088970

GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCATGGGCC

49

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to: 734

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seq_documentation_block:
ID Q9Y4L5;
AC Q9 (TrEMBLrel 12
DT 01-NOV-1999 (TrEMBLrel 12
DT 01-NOV-1999 (TrEMBLrel 12
DE HYPOTHETICAL 26.2 KD PROTE
OS HOMO sapiens (Hunan).

CC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RA BASSI M.T., BANFI S., RIBO
"The European IMAGE consor
RT human gene transcripts.";
RL Submitted (JUN-1999) to th
RN SEQUENCE FROM N.A.
RA AUFFRAY C., ANSORGE W., BA
RA AUFFRAY C., SOUSTIKA A., LU
RT The European IMAGE consor
RT human gene transcripts.";
RL Submitted (JUN-1999) to th
DR EMBL; AL079314; CAB45280.1
KW Hypothetical protein.
FT NOM_TER
1
SQ SEQUENCE 232 AA; 26168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_229/rev x Q9Y4L5
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Quality:
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  seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9Y4L5
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 26.2 KD PROTEIN (FRAGMENT).
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUFFRAY C., ANSORGE W., BALLABIO A., ESTIVILL X., GIBSON K., LEHRACH H., POUSTKA A., LUNDEBERG J.;
"The European IMAGE consortium for integrated Molecular analysis human gene transcripts."
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL079314; CAB45280.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASSI M.T., BANFI S., RIBONI M., BALLABIO A., "The European IMAGE consortium for integrated human dene transcripte "."
                                                                                                                                                                                                                                                                                                                                                                                                          196 GATAATCGAATGAAAAGTCACATTCCCGACAGACTCATCGCTCCTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                     54
                                                                                                                                                     39
                                                                                                                                                                                                          96
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                                                                                                                                                                                                                                                                                                                                                             27
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                                                                                                                                                                                                                                                                                                       CACCTCAGGATAAAGTTGTCATCTATGATGTCGACCTCTACTTTTTGAGG
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                                                                                                                                                                                                     AGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCCCA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 455
                                                                               CGGCGACGACTAGGGTCGTCGCGCCCAGGAGGACGACCATCA 2
                                                                                                                                                                                                                                                                                                                                                          AspAsnArgAlaAsnGlu...ArgGlyHisGlnThrHis......
                                                  ArgTyrArgSerArgGlySerSerArgProAspArgSerProAla 68
                                                                                                                                                     .....ThrAspPheTrpGlyAlaArgProProArgLeuProLeuGlyArg
sp_invertebrate:P91232
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43.077
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26168 MW; A8DF2B4D CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 232
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2
29.231
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seq_documentation_block:
ID P91232
AC P91233;
DT 01-MAY-1997 (TIEMBLIE
DE COSMID F08D12.
GN F08D12.
GN F08D12.
GN F08D12.
CRAMING FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718;
RX MEDLINE; 94150718;
RA WILSON R. AINSCOUGH
RA WILSON R. AINSCOUGH
RA WILSON R. JORAR S.,
RA GARDNER A., KERSHAW J.,
RA LIGHTNING J., LLOYD C
RA PARSONS J., EMENSTOCK
RA THIERRY-MIEG J., THON
RA THIERRY-MIEG J., THON
RA THIERRY-MIEG J., THON
RA THIERRY-MIEG J., THON
RA WATSON A., WEINSTOCK
RT 2.2 Mb of contiguous
RT elegans.";
RL
STRAIN-BRISTOL N2;
RA [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTON R.;
RL SUBMITTED (DEC-1996)
DR SEQUENCE 500440; AAB; 35
Sept 550
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                documentation_block:
O64410 PRELIMINARY;
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BONFIELD J., BURTON J., CONNELL M., COPER T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUUDERS D., SHOWNKEEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                064410;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
CYTOCHROME P450 MONOOXYGENASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
            Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 CCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE T., WATERSTON R.;
Submitted (DEC-1996) to the
EMBL; U80840; AAB37931.1;
PFAM; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TIEMBLIEL 03,
01-MAY-1997 (TIEMBLIEL 03,
01-NOV-1999 (TIEMBLIEL 12,
COSMID F08D12.
Poaceae; Zea
                                                                                                                                                                                                                                                                                                                                                                                    188 TCGATTATCAAAAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LeuThrAsnGlnGluGluIleArgLeuAspValLysThrAspArgPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 p...ArgTrpAsnLeuAsnPheCysGluIleAlaAsnValThrTyrThrV 98
                                                                                                                                                                                                                                                                                                                                    alGlyTyrGlnGln
                                                                                                                                                                                                                                                                                       sp_plant:064410
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2.241
71.053
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                   PRT;
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. Identity:
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alignment_scores:
Quality:
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    Quality:
    Ratio:
Percent Similarity:
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                                                                      alignment_block:
US-09-240-675-1_COPY_27_229 x 002424
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Percent Similarity:
                                          Align seg 1/1 to: 002424 from: 1 to: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
002424 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
YEGHIAZARYAN K., STRATER T., HACHTEL W.;
SUBMITTED (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ004810; CAA06156.1; -.
MENDEL; 28451; Zeama; 3078; 28451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   002424
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                                                                                                                                                                                                                                                                                                  YANDELL M.D., ROSS R.M., SUZUKI Y., WOOD W.B.; "Characteristics of dbl-1, a C. elegans decapentaplegic homologue, support a conserved role for BMP-family signaling in bilaterian development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TIEMBLIEL. 04, Created)
01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
DECAPENTAPLEGIC PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 TGTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTTCCACCTGCGGCT
                                                                                                                                                                                                            PRINTS; PRO0438; GFCYSKNOT.
SEQUENCE 365 AA; 41768 MW;
                                                                                                                                                                                                                                      Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF004395; AAC27729.1; -. HSSP: P18075; 1BMP. HSSP: P18075; 1BMP. PFAM; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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NON_TER 270
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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29 rgGlyGlyAlaPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 CAGGAGGACGACCA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 tSerSerAlaArgIleGlyProAlaArgProGlyLeuGlyAlaLysArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GCGGACAACACCCATGGGCCCACGGCGACGAGCACTAGGGTCGTCGCGCC
27 GACCCTAGTGGTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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2.857
55.263
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1.818
61.111
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                                                                                                                    Length: 54
Gaps: 2
Percent Identity: 29.630
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                                                                                                                                                                                                            7D3FDF49 CRC32;
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1
36.842
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               76
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Seq_documentation_block:
ID Q23047
AC Q23047
DT Q1-NOV-1996 (TYEMBLIZE DI Q1-NOV-1999 (TYEMBLIZE D1-NOV-1999)
CS Caenorhabditis elegan QC Evaryota; Metazoa; N QC Evaryota; Metazoa; Metazoa; N QC Evaryota; Metazoa; Metazo
                                                                                                                                                                                                                               alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_229 x Q23047
                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1996) to the ENBL; U64856; AAB04986.1; -. HSSP; P18075; IBMP. PFAM; PF00019; TGF-beta; 1. PRINTS; PR00438; GFCYSKNOT. SEQUENCE 379 AA; 43881 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTING J., LLOYD C., MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPBA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T25F10.2.
Caenorhabditis elegans.
Caenorhabditis elegans.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
27 GACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGT
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                                                                                                                                                                                                                                   Percent
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                                                                                                                                                                                                                                   Identity:
                                                                   379
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
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splleArgTrpThrLys

402

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seq_name: sp_rodent:Q60805
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US-09-240-675-1_COPY_27_229 x Q60805
                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                             Align seg 1/1 to: Q60805 from: 1 to: 994
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HSSP; P06213; 11...
MGD; MGI:99965; Mer.
A PFAM; PF00041; f13; 2.
PFAM; PF000047; f13; 2.
PFAM; PF000069; pkinase;
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01-NOV-1996 (TIEMBLIE). 01, Last sequence update)
01-NOV-1999 (TIEMBLIE). 12, Last annotation update)
01-NOV-1999 (TIEMBLIE). 12, Last annotation update)
C-MER PROTOONCOGENE PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
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GRAHAM D.K., BOWMAN G.W., DAWSON T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
                                                                                                                                Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U21301; AAA80222.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and developmental expression analysis of the tyrosine kinase."; Oncogene 10:2349-2359(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-B6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-315 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q60805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNODGRASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                              93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nThrGlyAsnSerGluArgLysAsnArgLysLysGlyArgLysHisHis.
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                                                        lAlaProLeuAsnIleThrValPheLeuAsnGluSerAsnAsnIleLeuA 397
                                                                                            ATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....AsnThrGluAlaGluSerAsnLeuCysArgArgThr 267
                                                                                                                                                                       GCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAA
                                                                                                                                                                                                                                                                                                                                                Quality:
.AGGTGGAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                          21
994 AA;
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2.222
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                        20 POT
994 C-N
110156 MW;
                                                                                                                                                                                                                                                                                                           Percent
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
C-MER TYROSINE KINASE RECEPTOR.
W; 3C2F429D CRC32;
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                                                                                                                                                                                                                                                                                                           Identity:
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33.333
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seq_documentation_block:
ID 097519;
AC 097519;
DT 01-NOV-1999 (TrEMBLrel. 12
DT 01-NOV-1999 (TREMBLrel. 12
DT 01-NOV-1999 (TREMBLREL. 12
DE TRANSCRIPTIONAL ACTIVATOR
GN SRCAP.
OS Homo Sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99278407.
RA JOHNSTON H., KNEER J., CHA
RT "Identification of a novel
RT which interacts with CREB-
RI J Biol. Chem. 274:16370-1
DR EMBL; AF143946; AAD39760.]
SQ SEQUENCE 2971 AA; 31563
Seq_documentation_block:
ID Q9YEB6;
AC Q9YEB6;
AC Q9YEB6;
DT 01-NOV-1999 (TrEMBLrel. 12,
DE 108AA LONG HYPOTHETICAL PRO
GN APEO658.
OC Archaea; Crenarchaeota; Aer
RN (1]
CARCHARA N.A.
COC ARCHARASHI M., SE
RRA SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE; 99310339.
RX MEDLINE; NAGURA N., SE
RA HOSOYAMA M., FUKUI S., NAGURA HOSOYAMA N., FUKUI S., FUKUI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-240-675-1_COPY_27_229/rev x Q9Y5L9
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JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIUK P., CHRIVIA J.;
JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIUK P., CHRIVIA J.;
"Identification of a novel SNF2/SWI2 protein family member, SRCAP,
which interacts with CREB-binding protein.";
J. Biol. Chem. 274:16370-16376(1999).

EMBL: AF143946; AAD39760.1;
EMBL: AF143946; AAD39760.1;
SEQUENCE 2971 AA; 315639 MW; 1C7B94CB CRC32;
                                            "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP000060; BAA79630.1; -.
                                                                                                                                                                                            MEDLINE: 9310339.

KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y., JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H., HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H., TAKAMIYA M., MASUDA S., FUWAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y., NOMURA N., SAKO Y., KIKUCHI H.;
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01.NOV-1999 (TrEMBLrel. 12, Last
01.NOV-1999 (TrEMBLrel. 12, Last
TRANSCRIPTIONAL ACTIVATOR SRCAP.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
108AA LONG HYPOTHETICAL PROTEIN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 TTTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rThrThrAlaValProAlaProThr 966
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3.333
72.000
            BAA79630.1; -
AA; 11371 MW;
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Last annotation update)
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                BCB1E741 CRC32;
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alignment_scores:
Quality: 59.50
Ratio: 2.705
Ratio: 2.705
Percent Similarity: 62.857
Percent Identity: 42.857

alignment_block:
US-09-240-675-1_COPY_27_229 x Q9YEB6
12 CCTCCTGGGGGGGGACACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGT 61
||||||:::|| :::|||
13 ProProSerArgProSerPro........GlnArgGlyProGlnGlyVa 26
62 TGTCCGCAGCCGAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAG 111
||||| :::||||
26 lPheGlyAlaCysArgGlyProGlnProLeuGlnSerArgArgSerArgG 43
112 GTCGA 116
|||||||
43 lyArg 44
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Result
No.
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Maximum DB seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                        114.5
111
95.5
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222.5
203
184.5
151.5
149.5
149.5
131.5
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Match
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1196
1 MMYVLLGATTLVLVAVGPWV......WKIGVYSPVHCIKTTVENEL 229
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                          88
                   R62023
R14643
R14663
W41803
R57138
W41804
W17734
W17734
W17734
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       Gamma interferon r
Mouse II-10 recept
Interleukin-10 rec
Human II-10 recept
Interleukin-10 rec
Human truncated ti
Human tissue facto
Sequence encoded b
Truncated tissue f
                                                                                                                                               Human cytokine rec
Human cytokine rec
Gamma interferon r
Gamma interferon r
Extracellular doma
                                                                                                                                                                                                                                          Human interferon r
Human IrN receptor
Spliced-deleted in
Spliced-deleted in
Transmembranal int
CRFB4 prottein. New
IFN-gamma receptor
                                                                                                                                                                                                                                                                                                                                               Soluble interferon
Sequence of a soul
IFN receptor extra
Human alpha-interf
                                                                                                               Plasmid pBABLUE hu
Gamma-IFN-R-GBP 13
Soluble human inte
                                                                                                                                                                                                         Human IFN-gamma ac
IFN-gamma receptor
                                                                                                                                                                                                                                                                                                                         Complete interfero Sequence of a soul
                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                               IFN-gamma receptor
Zcytor7 cytokine r
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## ALIGNMENTS

RESULT R28495 ID R AC R AC R	Db Oy	оу Оу Оу	X B O	 ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט	RESULT R14487 ID R AC R AC R DT 1 DE S KW I OS H
LT 2 95 R28495 standard; Protein; 436 AA. R28495; 31-MAR-1993 (first entry)	121 TPERKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSETYSLLIWKNSSGVEERI 180 [		Query Match 100.0%; Score 1196; DB 1; Length 436; Best Local Similarity 100.0%; Pred. No. 2.6e-115; Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps	и во чененск	LT 1 87 87 R14487 standard; Protein; 436 AA. R14487; 16-JAN-1992 (first entry) Soluble interferon-alpha/beta receptor. IFN; autolimmune disease; graft rejection; histocompatibility. Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mater soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosyppressants, for treating auto:immune and diseases and transplant rejection

If all 1: Styl : English.

NA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate coligonucleotides as primers and cloned CDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos C 030534 and 030535 R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for toxic side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                    16-SEP-1994; E03114.
16-SEP-1993; EP-402279.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE S)
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
N-PSDB; 086457.
Compsn. of monoclonal antibodies against interferon useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English. A recombinant soluble form of the human interferon c protein extracellular domain, given in R71723, was 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1992.
17-APR-1991; WO-F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eid P. Gresser I, Lutfalla G, Mc
                                                                                                                                                                                                              16-OCT-1995 (first entry)
IFN receptor; interferon receptor; interferon receptor; interferon receptor; interferon receptor; interferon receptor; interferon-beta; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                    Homo sapiens.
WO9507716-A.
                                                                                                                                                                                                                                                                                R71723 standard; Protein; R71723;
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                                                                                                                                                                                       New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis Disclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residues 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
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20-OCT-1999; FR-013770.
(CNRS) CNRS CENT NAT RECH SCI.
MOGENSEN KE, UZE G, Lutfalla G,
WPI; 91-148740/20.
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Human alpha IFN; IFN
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R11958;
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IFN; IFN agonists; antiviral;
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05-FEB-1990;
05-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.
The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also 014239.
31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                               R28496;
R28496;
31-MAR-1993 (fir
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N-PSDB; Q14240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease,
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disease; graft rejection;
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06-OCT-1993.
31-MAR-1992; 4
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neutralising activity a
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                                                                                                                                                         EP-400902
                                                                                                                                                                                400902.
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     against
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29-OCT-1992.
17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
EId P, Gresser I, Lutfalla G, Meye
Tovey M, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases and transplant rejection
Claim 3; Fig 2; 58pp; English.
DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonuclectides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos 230534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids. Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune
                                                                    (EUBI-) LAB EURO BIOTECHNOLOGIE Benoit P, Maguire D, Meyer F, WPI; 93-312951/40.
                                                                                                                                                                                                                                                                                                                                                      IFW.R; extracellular domain; monoclonal antibody; viral in cell proliferation; allograft rejection; systemic lupus er psoriasis; multiple sclerosis; Behcet's Disease; aplastic immunodeficiency; measles virus; interferon-alpha-beta.
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1. .436
                                                                                                                                                                                                                                       /label= extracellular_domain
/note= "soluble, immunogenic
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Pred. No. 3.7e-115;
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Best Local S
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Matches 22
                                                                                                                                                Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.

The amino acid sequence of human interferon class I receptor is given in R73356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IRN-sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                   Human IFN receptor: Interferon receptor; interferon-beta; monoclonal antibody;
                                                                                                                                                                                                                                                                                          23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
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Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                         MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
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FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                              MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                            229;
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Pred. No. 3.7
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No. 3.7e-115;
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1.7e-115;
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Matches 228; Conser
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(ABRA/) ABRAMOVICH C.
Abramovich C. Ratovitski
WPI: 95-200634
                                                                                                                                                                                                                                                                                                                                                                                           Novel splice-deleted interferon alpha-receptor (IRNAK) LULIM A (W21805) is characterised by a new domain (5) which follows an end-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U366 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN the response of human cells to IFNS, either by acting as IFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1997 (first entry) Spliced-deleted interferon Interferon alpha-receptor;
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                                                                                                                                                                                                                                                                                                                                           antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhe modulate or modify the activities of IFNs alpha and beta in ce tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mammalian soluble interferon alpha-receptor forms inhibiting, modulating or modifying the activities of i Example 2; Fig 7; 46pp; English.
Novel splice-deleted interferon alpha-receptor (IFNAR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1994;
24-OCT-1993;
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                ENIYSRHKIYKLSPETTYCLKYKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                          TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
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ENTYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                             TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
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                                                                                                                                                                                                                                                   Conservative
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/note= "comprises amino acids
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Pred. No. 8.4e-115;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                Length 434;
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interferon(s)
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RESULT W21806

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Novel splice-deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T73521) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms,
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Matches 228
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11-MAY-1995.
20-OCT-1994;
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(YEDA) YEDA RES & DEV CO
(ABRA) ABRAMOVICH C.
                                        23-SEP-1997 (first entry)
Transmembranal interferon alpha-receptor;
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Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abramovich C, Ratovitski E,
WPI; 95-200634/27.
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W21806;
                                                                                                     W21804 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interferon alpha-receptor;
                             Homo sapiens.
                                                                                                                                                                                181
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                                                                                                                                                                                                                                                        TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                          MYVLLGATTLYLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                ENIYSRHKIYKLSPETTYCLKVKAALLISWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                ENTYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                          TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                    FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                  FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .419
/label Extracellular_domain
/note- "comprises amino acid residues 1-413
422-427 of transmembranal IFNAR"
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/label Intracellular_domain
/note "comprises amino acids
transmembraņal IFNAR"
Location/Qualifiers
1. .436
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                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%;
                                             alpha-receptor.; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496
                                                                                                       557
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1191; DB 1;
Pred. No. 1e-114;
0; Mismatches 1;
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Best Local :
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                                                                              22-JAN-1998.
17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
KOtenko SV, Pestka S;
WPI; 98-110590/10.
N-PSDB; V19874.
New recombinant DNA - com
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11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES 6 DEV CO L
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting, modulating or modifying the activities of interferon(s Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
Claim 2; Page -; 79pp; English.

This sequence is the human CRFB4 sequence, DNA encoding it is used recombinant DNA (1) of the invention. (1) comprises a sequence (Sl) encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence
                                                                                                                                                                                                                                               CRFB4; interle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abramovich C, Ratovitski E, WPI; 95-200634/27
                                                                                                                                                                                                                    septic shock; immune response;
                                                                                                                                                                                                                                                                            23-JUN-1998
                                                                                                                                                                                                                                                                                        W52296 standard;
W52296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian soluble interferon alpha-receptor
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                                                        rejection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                    interleukin-10; IL-10; IL-10 receptor; allograft rejection;
photosensitivity; inflammation; autoimmune disease;
shock; immune response; organ rejection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Extracellular_domain 437. .457
                                                                 DNA - comprises sequences encoding interleukin-10 to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label-
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                                                                                                                                                                                                                                                                                                     Protein;
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Pred. No. 1.2e-114;
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les of interferon(s)
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    B
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C Cells containing (I) may be used to identify agonists/antagonist of C II-10. Agonists are potentially useful, e.g. for preventing allograft CC rejection, as vaccine adjuvants, for treatment of photosensitivity, confilammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, viruses, bacteria and parasites (especially intracellular pathogens) and CC restore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit II-10 activity in cells. Antibodies specific for CRFB4 are used to measure and localise CRBF4, for diagnosts of defective II-10 activity. Fragments of (I) are used as primers or probes to assay CRFB4-specific CC RNA. Agonists/antagonists may be administered parenterally, orally or rectally especially by intravenous injection or directly into a tumour or callograft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 66
Novel interferon gamma receptor beta chain p
treatment of inflammatory bowel disease and
Claim 3; Fig.2A; 86pp; English.
The IFN-gamma receptor beta-subunit encoded
                                                                                                                                                                                                                                                                                                                                                                               IFN-gamma receptor beta-subunit.
Interferon-gamma receptor beta s
interferon-gamma-antagonist.
                                                                              (HEMM/) HEMMI S.
Aguet M, Boehni R,
WPI; 95-224321/29.
                                                                                                                                                        15-JUN-1995.
07-DEC-1994; U14277.
09-DEC-1993; US-164596.
                                                                N-PSDB; Q90808
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                                                                                                                            (AGUE/) AGUET M.
(BOEH/) BOEHNI R.
                                                                                                                                                                                                                                                                                                                                     peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                   'label Sig_peptide
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                                                                                                Hemmi
                                                                                                                                                                                                                         Cytoplasmic_domain
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Pred.
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No. 4.7e-15;
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                                 chain polypeptide ase and liver damag
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    a cDNA clone
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                                                 Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful proven human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases Claim 1; Pages 55-59; 72pp; English.

Claim 1; Pages 55-59; 72pp; English.

This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-cytokine receptor family (CRF2). An expression vector containing the Zcytor polynucleotide, operably linked to transcription promoter, a sequence polynucleotide, operably linked to transcription promoter, and a cencoding a transmembrane and intracellular domain, or both, and a croombinant production of the polypeptide. The sequences can be used to transcriptional terminator can be used to transform host cells for the recombinant production of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor7 can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.NOV-1998 (first entry)
20.NOV-1998 (first entry)
20.YOY-1998 (first entry)
20.YOY-7 cytokine receptor polypeptide.
20.YOY-7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
20.YOY-7; cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
agonist; cell proliferation; cell differentiation; renal disease; human;
neural disease; pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from mouse B-cells is given in R75782. Recombinant beta-
pref. with the transmembrane anchoring domain deleted or
inactivated and with the cytoplasmic domain deleted, may
may be used to treat pathological conditions associated w
IFN-gamma production.
                                     also be used in the treatment of renal,
                                                                                                                                                                                                                                                                                                                                      N-PSDB; V57515.
                                                                                                                                                                                                                                                                                                                                                                       Adams RL, Fa. Whitmore TE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
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ZYMOGENETICS INC.
L, Farrah TM, Jelmberg
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sequence claimed in claim 1"
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Pred. No. 4.9e-13;
8; Mismatches 86
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.7%; Score 151.5; DB 1; Length 337; Best Local Similarity 24.6%; Pred. No. 1e-07; Matches 61; Conservative 44; Mismatches 94; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suppressing tumours in mammals with accessory factor 1 (AF-1) -
for interferon gamma, specifically induction of class I HLA
antigens, including use of AF-1 DNA in gene therapy
Disclosure; Fig 21A; 114pp; English.
The sequence is that of human interferon-gamma accessory factor-1.
Incorporation of AF-1 into immune and tumour cells re-establishes
normal function with elimination of malignant cells.
Sequence 337 AA;
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COOK JR, Donnely RJ, Emanuel S,

Pestka S, Schwartz B, Soh J;

WPI; 95-106679/14.

N-PSDB: 084697.
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22-AUG-1994; U09438.
20-AUG-1993; US-110119.
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Human IFN-gamma accessory factor-1.
Interferon-gamma; AF-1; tumour.
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  219 HCIKTTVE 226
                                           175 YYVHYWE--KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI 232
                                                                                     165
                                                                                                                           120 GALHSAWTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRESSPEDIADTSTAF----EC 174
                                                                                                                                                                    109 ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT 164
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                                                                                                                                                                                                            YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL 119
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                                                                                   YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV 218
                                                                                                                                                                                                                                                                                                LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFK 68
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Search completed: June 1, 2000, 00:40:15 Job time: 20021 sec

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Title:
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138.798 Million cell updates/sec
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Sequence 11, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 26, Appl Sequence 27, Appl Sequence 36, Appl Sequence 37, Appl Sequence 38, Appl Sequence 41, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Sequence 43, Appl Sequence 44, Appl Sequence 44, Appl
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Query M Best Lo Matches	Sequence 11, Sequence 11, Sequence 11, Patent No. 566 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF I COMPUTER OF COMPUTER: 20 OPERATION SOFTWARE CURRENT AP APPLICAT FILING D PRIOR APPLICAT FILING D PRIOR APPLICAT APPLICAT APPLICAT APPLICAT FILING D APTORMATION SOFTWARE CURRENT AP APPLICAT TITLECOMMUN TELEFERNO TELEFERNO TELEFAX: INFORMATION SEQUENCE C LENGTH: SEQUENCE C SEQUENCE C STRANDEL TOPOLOGY MOLECULE 1 S-08-328-256-1		00000000000000000000000000000000000000
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                                                           Best Local Similarity Matches 229; Conserv
                                                                                            Query Match
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TITLE OF INVENTION:
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US,
FILING DATE: 05-DEC-19
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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                                                                                                                                                                         TOPOLOGY:
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3000 K Street, N.W.,
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PLAVEC, Ivan
TOVEY, Michael G.
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MEYER, Francois
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                                                                                                                                                                                                                                                                                     28,665
FR: 17283/117/GUPL
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                                                             Score 1196; DB 2;
Pred. No. 2.4e-126;
Mismatches 0;
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                                                                                       Length
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RESULT 3
US-08-328-256-12
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GENERAL INFORMATI
                                                                                                                    Matches
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                                                                                                                                  Best
                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: REVEL-1
REFERENCE/DOCKET NUMBER: 25.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/328
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 496 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS SOCTWARE: PATENTIN RE-BASE #1.0. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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              61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
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                                                                                                                                  Local
                                                                                                                                                                                                                                                       TYPE:
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                                                       TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERI 180
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                                                                                                                  l Similarity
229; Conserv
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419 Seventh Street, N.W., Suite 300
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                                                                                                                  Conservative
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linear
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                                                                                                                 Score 1196; DB 1;
Pred. No. 3e-126;
); Mismatches 0;
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US-08-328-256-10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: REVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                     FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
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                                                                                                                                                                                          MAVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVT 60
                                   TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                        MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
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SYSTEM: PC-DOS/MS-DOS
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24-OCT-1993
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Pred. No. 3.6e-126;
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Matches
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY,AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
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APPLICANT: GRESSER,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin RelacTION DATA:
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 181
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                                                                                                                                     61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
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SOFTWARE: Patentin
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                                                                                                     FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                      MYVYLLGATTLVLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                     TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                        100.0%; Score 1196; DB 1; 100.0%; Pred. No. 3.6e-126; tive 0; Mismatches 0;
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LENGTH: 557 amino acids
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APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                  Local
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   181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/O FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                   61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BYRNE, THOMAS E
                                                                                                                                                                                                  1 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                                                                 MYVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                    FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
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5861258
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LUTFALLA, Georges
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THE ALPHA INTERFERON RECEPTOR AND
PREPARATION OF THE CORRESPONDING I
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
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SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
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TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
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TELEX: 200797 NIXN UR
TELEX: 200797 NIXN UR
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                                                                                                                                                                                1 MYVYLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
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ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                     TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
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    Application US/0847145;
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EM: PC-DOS/MS-DOS
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1-1992
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Pred. No. 3.6e-126;
; Mismatches 0;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4
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Patent No. 5919453
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acid
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
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APPLICATION NUMBER: EP 9:
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
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121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
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                                                                                                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                               TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
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TOVEY, Michael G.
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PLAVEC, Ivan
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100.0%; Pred. No. 3.6e-126;
tive 0; Mismatches 0;
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                                                             US-08-683-743-4
            Sequence 4, Application US/08683743 Patent No. 5843697 GENERAL INFORMATION:
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; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-14277-3
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 202 amin
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 08/164596
APPLICATION UNMBER: 09/164596
FILLING DATE: 09-DEC-1993
ATTORNEY, AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PAtth (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
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181 PSLKKHSNYSTXQCISTTVANK 202
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                                                                                                                                                                    88 NFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                                                                                                                            28 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                                                                                                                                                                                     Local Similarity
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                           LTSWKIGVYSPVHCIKTTVENE 228
                                                                                                                                                EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                                                                         SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                           SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
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                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                   41.0%; Score 490.5;
48.5%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor
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                                                                                                                                                                                                                                                                                                                     1.9e-47;
                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                    PCT-US94-14277-2
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                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-343-1684
NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: V/VC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-UUL-1996
FILING DATE: 17-UUL-1996
FILING DATE: 135
FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                             CORRESPONDENCE ADDRESS:
                                                                                                         TITLE OF INVENTION: Receptor Subunit Polypeptides NUMBER OF SEQUENCES: 8
                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        176 EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 30.3 hes 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 WVLSAAAGGKNLKS------PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAOIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 411 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
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                            460 Point San Bruno Blvd

    David A. Jackson, Esq.
    Hackensack Ave, Continental Plaza,

                                                                                                                                                       Bohni, Ruth
Hemmi, Silvio
                                                                                                                                                                                                                 Aguet, Michel
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/ENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                Inc.
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Pred. No. 5.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-US94-14277-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
ZIP: 94080
COMPUTER REALABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Aguet, Michel APPLICANT: Bohni, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 352 _____
TYPE: amino acid
Tinear
                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YENVTVGPPKNISVTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                     Bohni, Ruth
Hemmi, Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.0%;
                                                                                                                                                                                                                                                                                                                                            Receptor Subunit Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 203; DB 4;
Pred. No. 9.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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86;

Gaps

13;

184

Length 332; Indels 36;

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RESULT 13
US-08-943-087-2
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Best Local Similarity 29.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08943087 Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                       CURRENT APPLICATION DATA
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Love, Richard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 KPYRVYCLQTERQLILKNKKIRPHGLLSNVSCHETT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
                                                     OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                     COMPUTER: IBM Compatible
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                 ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ropology:
                  APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NITSTKCNESS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H: 223 amino acids amino acid
                                                                                                                                                                                                   Seattle
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                                                                                                                                                                                                                    1201 Eastlake Avenue East
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                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                               Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                   Lok, Si
Kho, Choon J.
                                                   SYSTEM: DOS
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                          ZymoGenetics, Inc
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                                                                                                                                                                                                                                                                                                                                Theodore E
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Pred. No. 8.5e-14;
7; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 223;
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; FRAGMENT TYPE:
US-08-943-087-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/80 FILING DATE: 20-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                      APPLICANT: FAIRTAH, Theresa M.
NITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 QCVTN----HTLVLTWLEPNTLYCVHVES 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 QIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LVLVAVGPW--VLSAAAGGKNLKSPOKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYOK 67
CLASSIFICATION:
                                                                                                                                                                 COUNTRY: UZIP: 98102
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REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                  Seattle
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Kho, Choon J.
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Ol Eastlake Avenue East
                                                                                                                         Diskette
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                                                                                                                                                                                                                                                                                                                                                 Theodore E.
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Pred. No. 2.4
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es 95;
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Length 553; Indels

21;

Gaps

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 20-FEB-1997

08/803,305

ORNEY/AGENT INFORMATION:

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US-08-943-087-16
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Best Local Similarity 26.3
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11: MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                 APPLICANT: FAIRSH, THERESA M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 QCVTN----HTLVLTWLEPNTLYCVHVES 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204 : : | | | | | | | : : :
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                                                                                                                                                                                                                        STREET: 1201 :
CITY: Seattle
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                                                                                                                                                                                                               STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                   FILING DATE:
                                                  APPLICATION NUMBER:
                                                                                                                                                                             COUNTRY: U
ZIP: 98102
                                                                                                                                                                                                                                                                    ADDRESSEE:
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DR APPLICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08943087
                                                                                                                                                                                                                                               E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                               Lok, Si
Kho, Choon J.
                                                                                                                                                                                              USA
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Adams, Robyn L.
Whitmore, Theodore
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internal
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                                                                                                                                                                                                                                                                                                                                                          Theodore E.
                                                 US/08/943,087
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; FRAGMENT TYPE:
US-08-943-087-16
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Best Local Similarity
Matches 55; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
196 QCVIN----HTLVLTWLEPNTLYCVHVES 220
                                   178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
                                                                     136 QIGPPEVALTIDEKSISVYLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNIKSNRIWS 195
                                                                                                       127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                 11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                             76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                             68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                   18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-442-6678
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internal
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                                                                                                                                                                                                                                                                                         38;
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Pred. No. 2.4e-12,
18; Mismatches 91
                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                           Length 553;
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Gaps

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Search completed: June Job time: 15449 sec ۳ 2000, 04:17:55

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Result
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Listing first
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Maximum DB seq length: 1000000
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Perfect score:
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C;Genetics:
A;Gene: GDB:IFNAR; IFRC
A;Gene: GDB:IFNAR; IFRC
A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: cytckine receptor; glycoprotein; transmembrane protein
E;1-21/Domain: transmembrane #status predicted <TRN1>
E;437-455/Domain: transmembrane #status predicted <TRN2>
E;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lutfalla, G.
submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor gene.
A;Reference number: S17112
A;Accession: S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon alpha/beta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C;Accession: A32694; S17112
R;Uze,.G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into mouse
A;Reference number: A32694; MUID:90124632
A;Accession: A32694; MUID:90124632
A;Accession: A32694
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A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross_references: EMBL:X60459; NID:g32671
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A;Residues: 1-557 <UZE>
A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1;
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                                                                                                                 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERI 180
                     ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                         TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
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interferon alpha/beta receptor - mouse (C;Species: Mus musculus (house mouse) C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Accession: A4528; 148423; 148424; 148425; 148426; 148427; 148428; 148429 R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A;Reference number: A45283; MUID:92262522
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A; Molecule type: mRNA
A; Residues: 1-421,'V',423-560 <LIM>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
C;Accession: Ltfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
FEBS Lett. 313, 255-259, 1992
                                                                                                                                         A; Residues: 1-590 <UZE>
A; Residues: 1-590 <UZE>
A; Cross-references: GB: M89641; NID: g194111; PIDN: AAA37890.1;
A; Cross-references extracted from NCBI backbone (NCBIN: 102354)
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A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:I-24/Domain: signal sequence #status predicted <SIG>
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A;Title: Cloning and characterization of a
A;Reference number: S33770; MUID:93305725
A;Accession: S33770
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A; Residues: 1-560 < MOU>
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                           A; Title: St
A; Reference
                                                                                                  Gene 148,
                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: mRNA
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C;Species: Bos primigenius taurus (cattle)
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                   Structure of the murine interferon alpha/beta nce number: I48423; MUID:95047447
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                                                                                                  343-346,
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155; Conserv
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67.1%; Pred. No. 6.50
tive 31; Mismatches
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                                                       receptor-encoding gene:
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NCBIP:102357)
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A; Reference number: G06935
A; Accession: G01418
A; Status: pre] imi---
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from

GB/EMBL/DDBJ

April

06-Jun-1997

#text\_change

17-Jul-1998

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RESULT
G01418
cytokine receptor family II, member 4 - C;Species: Homo sapitens (man)
C;Date: 21-Dec-1996 #sequence_revision C;Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 177/3; 331/1
C;Keywords: cytokine re
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A; Status: preliminary; translated
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A; Residues: 127-224 <RE2>
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A; Residues: 473-590
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A; Residues: 426-445 <RE6>
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A; Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 265-375 < RE4>
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A; Residues: 118-1
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A;Status: preliminary; translated
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A;Residues: 243-264 <RE3>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLAVVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
                                                                                                                                                                          STYYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCISTTVANKM
                                                                                                                                                                                                                                                                                                                                                  SAEYRTKDEAKWLKVPECQHTTTTKCEFSLLDTNVXIKTQFRVRAEEGNSTSSNNEVDPF
                                                                                                                                                                                                                                                              IPFYTAHMSPPEVRLEAEDKAILVHISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTI
                                                                                                                                                                                                                                                                                                                                                                                           SFDYOKTGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSF 120
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Pred. No. 6.4e-45;
0; Mismatches 69
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cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
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C;Keywords: transmembrane protein
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A;Title: A new member of the cytokine receptor gene family maps on chromosome A;Reference number: A47003; MUID:93300510

A;Accession: A47003
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A; Residues: 1-273 <LUT>
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A; Residues: 1-325 <LUT>
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Best Local
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                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSLGSWLGGCLLVSALGMVPPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                          HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT
                                                                                                                              PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                                                                   WVLSAAAGGKNLKS------PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGMQVEVLDDSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF 175
                            EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT
                                                                                              PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                               YRIFODKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                               NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                 WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
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                                                                                                                                                                                                                                                                                                      66;
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Pred. No. 1.2e-12;
2; Mismatches 91;
                                                                                                                                                                                                                                                                                                                      Score 222.5; DB 2
Pred. No. 4.2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: A novel member of the interferon A; Reference number: A49947; MUID: 94170381 A; Accession: A49947
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R;Hemm1, S.; Bohn1, R.; Stark, G.; Di Marco, Cell 76, 803-810, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
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A; Residues: 1-349 <GIB>
A; Cross-references: GB: U53696
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Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JC6311
R;Gibbs, V.C.; Pennica, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-332 <HEM>
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A; Accession: JC6311
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Best Local
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                                                  123 FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 VHLEAEDKAIVIHIS------PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENI 183
                                                                                                                                                        71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                             16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                   21 LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 -----CKRTASTQCDFS--HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 VGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNW 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDSEVLRNLEPWTTYCIQVQGFLLDQNRTGEWSEPICERT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MQIESLAESLELRFSAPQIENEPET-----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSP
                                                                                                     DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
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                                                                                                                                                                                                                                                                                                                                                  Score 203; DB 2;
Pred. No. 2.2e-10;
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Pred. No. 7.6e-12;
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-VFHGATFQYLVHYWEKSETQQEQVE
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184
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RESULT 9
A31555
A31555
Interferon gamma receptor precursor - human
C; Species: Homo sapiens (man)
C; Date: 28 Feb-1990 #sequence_revision 28-Feb-1
C; Accession: A31555
R; Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A; Title: Molecular cloning and expression of the A; Reference number: A31555; MUID:89003065
A; Accession: A31555
A; Molecule type: mRNA
A; Residues: 1-489 <AGU>
A; Cross-references: GB:J03143; NID:9184650; PII
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A; Residues: 1-63,'Q',65-337 <RE2>
A; Cross-references: EMBL:U05877;
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C;Genetics:
A;Gene: GDB:IFNGR1;
A;Cross-references:
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R;Soh, J.; Donnelly, R.J.; Kotenko, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-337 < RES>
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Best Local S
Matches 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                               SCYETMAD 240
                                                                                                                                                                                                                                                                                                                                                                                 HCIKTTVE 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLLGVFAAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENT-SSWYEVDSFTPFRKAQIGPPEVHLE----AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
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 GDB:120688;
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 OMIM: 107470
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Pred. No. 7.3e-06;
""" tches 94;
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                                                   PIDN: AAA52731.1;
                                                                                                                                           the
                                                                                                                                           human
                                                                                                                                           interferon-gamma receptor
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                                                 PID: 9306915
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A; Residues: 1-477 <COF>
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A; Residues: 1-477 < KUM>
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A; Map position: 6q23-6q24
C; Superfamily: interferon
C; Keywords: cytokine recep
                                                                                                                                                                                                                                                                   R;Hemmi, S.; Peghini, P.; Metzler, M.; Merlin, G.; Dembic, Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989 .
A;Title: Cloning of murine interferon gamma receptor cDNA: A;Reference number: A34508; MUID:90099370
A;Accession: A34508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:JOS265; NID:g197964; PIDN:AAA39178.1; R;Gray, P.W.; Leong, S.; Fennie, E.H.; Farrar, M.A.; Pingel, Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989
A;Title: Cloning and expression of the cDNA for the murine in A;Reference number: A34423; MUID:90046824
A;Scatus: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change
C;Accession: A34368; A35468; A34508; A34508; A36224; I48941
R;Kumar, C.S.; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.
J. Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular characterization of the murine interferon gam
                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-94,'E',96-477 <HEM>
A;Cross-references: GB:M28233; NID:g194131;
                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Acidues: 1-94,'E',96-477 <GRA>
A;Ressidues: 1-94,'E',96-477 <GRA>
A;Cross-references: GB:M26711; NID:g194126; PIDN:AAA37896.1; PID:g309330
A;Cross-references: GB:M26711; NID:g194126; PIDN:AAA37896.1; PID:g309330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M25764; NID:g197962; PIDN:AAA39177.1; R;Cofano, F:; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis, and cDNA sea;Reference number: A35468; MUID:90154099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A34368; MUID:90036866 A;Accession: A34368
R;Munro, S.; Maniatis, T.

Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
A;Title: Expression cloning of the murine interferon gamma
A;Reference number: A36224; MUID:90083245
A;Accession: A36224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 ALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA---EKENTSSWYEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEY--QIMPQVPV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVLLGATTLYLVAVGPWVLSAA-AGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNV-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSFTPFRKAQIGPPEVHLEAEDKAIVIHI --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEFAVCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKE--SAYAKS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EDDCDEIQCQLAIPVSSLNSQYCVSAEGVL
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%; Pred. No. 0.0
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                   PIDN: AAA37898.1;
                                                                                                                                                                                                                                                                                                                                      receptor cDNA:
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                                                                                                                                                                                                                                                                                                                                   expression
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                                                            receptor cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g309394
J.T.; Ferna
                                                                                                                                                PID:g309331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g309393
S.; Appella,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandez-Luna, J
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                                                                                                                                                                                                                                                                                                                                      human
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cells

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A; Map position: 4
A; Introns: 10/3; 61/3;
A; Introns: 6883/3; 6768/1;
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A;Title: Characterization of the 5' flanking region and gene encoding the A;Reference number: I48941; MUID:95197006
A;Accession: I48941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-477 <MUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A;Reference number: Z20442 A;Accession: T27934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-28 < RES>
                                                                                                                                                                               A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                    A;Cross-references: EMBL:273899;
                                                                                                                                                                                                                                    A; Residues: 1-6831 <WI2>
                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, May 1996 A; Reference number: Z20458
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-6831 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 2K617.1a - Caenorhabditis elegans
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  Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
Accession: T27934; T28030
                                                                                                                                                                                                                                                                           Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                         :Cross-references: EMBL:273897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a:Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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y Match 8.2%;
Local Similarity 22.8%;
nes 44; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE-KENTSSWYEVDSFTPFRKAQIGPP--EVHLEAEDKAIVIHISP-----GTKDSVMWA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQ-----KTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIK-----LRIR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGRMILLVV--LMLSAKVGSGALTSTEDPEPPSVPVPTNVLIKSYNL-----NPVVCWE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTLVLVAVGPWVLSAAAGGKNLKS---PQKVEVDIIDDNFILRWNRSDESVGNVTFSFD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DGSTCYTFDYTYYVEHNRSG-----EILHTKHTVEKEECNETLCELNISVSTLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKVGQKESDYARSKEFLMCLKGKVGPPGLEIRRKKEEQLSVLVFHPEVVVNGESQGTMFG
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                                                                                                 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 6800/3
                                                                                                                                                                                                 clone
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22.9%;
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ZK829
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Pred. No. 0.23;
8; Mismatches
                  Score 97.5;
Pred. No. 21;
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    Mismatches
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                                      Length
    Indels
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    53,
  Gaps
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A;Map position: IV
A;Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/
152/3; 669/3; 6776/1: 6808/3
C;Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homol
C;Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; seri
F;806-898, 899-990, 991-1083,1084-1175,1178-1273,1474-1567,1770-1864,2066-2158,2358-2
96-5790,6263-6356,6386-6478,6541-6635,6649-6742,6745-6838/Region: motif 2
F;1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2
23,4215-4313,4314-4415,4416-4516,4612-4710,4711-4811,4908-5009,5010-5109,5110-5210,
F;5940-6197/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: myosin-regulating protein
N; Contains: protein kinase (EC 2.7.1.-)
C; Species: Caenorhabditis elegans:
C; Date: 28-Oct-1995 #sequence_revision 24-Oct-1997
C; Accession: $57242; $07571; $06797; $57218
R; Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
submitted to the EMBL Data Library, February 1993
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Experimental source: var. Bristol
C;Comment: Lack of unc-22 leads to a constant twitching of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics 134, 1097-1104, 1993
A;Title: Additional sequence complexity in the muscle A;Reference number: S57218; MUID:93387664
A;Accession: S57218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Experimental source: var. Bristol R; Benian, G.M.; L'Hernault, S.W.; M Genetics 134, 1097-1104, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Sequence of an unusually large protein A; Reference number: S06797; MUID:90044042 A; Accession: S06797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: var. Bristol R; Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Nature 342, 45-50, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-6839 <BEN1>
A; Cross-references: EMBL:L10351
A; Experimental source: var. Bri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S57242
A; Accession: S57242
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A; Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 792-6839 <BEN2>
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                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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A; Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7160 < W12>
A;Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
A;Experimental source: clone ZK829
A;Experimental source: clone ZK829
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submitted to the EMBL Data
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A;Cross-references: EMBL:Z73897;
A;Experimental source: clone ZK6
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A;Residues: 1-7160 <
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Best Local S
Matches 44
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Local Similarity 22.88;
Local Similarity 22.88;
hes 44; Conservative 2
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                    TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 141
                                                                                                                                                                                        LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP---CAKV 2241
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     CLKVKAALLTSWK 211
                                                                           IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY 198
                                          -GTPDVVDWDADRVS----LEWEPPKSDGG--
                                                                                                                                                                                                                                                                  Conservative
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Lys #status predicted
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Pred. No. 21;
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Pred. No. 22;
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7/1; 7129/3
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                                        APITOY 2322
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1995 #text_change 05-Nov-1999
C;Accession: A49667
                                                                                                                                                                                                                                         R;Gattung, S.; Scheet, P.; Kemp, K.
submilted to the EMBL Data Library, November 1996
A;Bescription: The sequence of C. elegans cosmid i
A;Reference number: 220647
A;Accession: 729585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;HO, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, i
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A;Title: A receptor for interleukin IO is related to
A;Reference number: A49667; MUID:94068585
A;Accession: A49667
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                   hypothetical protein F55F8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tcC;Accession: T29585
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A; Residues: 1-575 < RES>
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                                                                             A; Introns:
                                                                                                A; Map position:
                                                                                                                 A; Gene: CESP: F55F8.3
                                                                                                                                                    A;Cross-references: EMBL:U80447; PIDN:AAB37807.1; GSPDB:GN00019; CESP:F55F8.3
A;Experimental source: strain Bristol N2; clone F55F8
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-925 <GAT>
                                                                                                                                                                                                                         A; Status: preliminary; translated
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## INRL\_HUMAN STANDARD P17181; 01-AUG-1990 (Rel. 15, C 01-AUG-1990 (Rel. 15, L 15-FEB-2000 (Rel. 39, L MEDINE: 90124632. Uze G., Lutfalla G., Gresser I.; Uze G., Lutfalla G., Gresser I.; "Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA."; Cell 60:225-234(1990). PHÓSPHORYLATION BY TYK2. MEDLINE; 95059042. Colamonici O., Van H., Domanski P., Handa R., Smalley E Colamonici O., Witte M., Krishnan K., Krolewski J.; Mullersman J., Witte M., Krishnan K., Krolewski J.; "Direct binding to and tyrosine phosphorylation of the of the type I interferon receptor by p135tyk2 tyrosine for cell. Biol. 14:8133-8142(1994). -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. SEQUENCE FROM N.A. MEDLINE; 92129376. Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.; "The structure of the human interferon alpha/beta receptor gene."; J. Biol. Chem. 267:2802-2809(1992). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. +++ ---SEQUENCE FROM N.A. MEDLINE; 90124632. IFNAR1 OR IFNAR. 01-AUG-1990 (Rel. 15, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC). Cell. Biol. 14:8133-8142(1994). FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPH I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS. EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS. EYM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS. STANDARD; Created) 557 on of the alpha subunit tyrosine kinase."; Ö.

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EMBL; PIR; PIR; S

L; J03171; AAA52730.1; ... X60459; CAA42992.1; ... X32694 ... ... A32694 ... ... X327112; S17112; S17112 ... ... S17450; -..

EMBL;

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Eutheria; Cetartiodactyla; Ru
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MEDLINE; 93076908.

Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

"Specific antiviral activities of the human alpha interferons determined at the level of receptor (IFNAR) structure.";

FEBS Lett. 313:255-259(1992).
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Ruminantia; l
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G -> A (IN REF. 2).

G -> CRC64;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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MEDLINE; 93305725.

Lim J.-K., Langer J.A.;

"Cloning and characterization of a bovine alpha interferon receptor."

"Cloning and characterization of a bovine alpha interferon receptor."

Blochim. Blophys. Acta 1173:314-319(1993).

1 FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYP.

1 ITNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

SUBGUNITS THEMSELVES.

1. SUBGULULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1. SUBGULULAR LOCATIONS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

1. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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INR1_SHEEP
Q28589; Q95206;
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INTERFERON-ALPHA/BETA RE
(INTERFERON ALPHA/BETA F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pregnancy.";
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Endocrinology 138:4757-4767(1997).
Endocrinology RECEPTOR FOR INTERFERONS ALPHA AND BI
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND EN-
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A
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"Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaluz S., Fisher P.A., "Structure of an ovine endometrium.";
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Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; I
                  CONFL
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PFAM; PF00041; fn3; 1.
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TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED E
CONCEPTUS AT DAY 15 OF PREGNANCY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF
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                   17:207-215(1996).
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Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
A RECEPTOR-1).
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A -> D (IN REF. 2).
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BY SIMILARITY.
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"Behavior of a cloned murine interferon alpha/beta receptor expressed
in homospecific or heterospecific background.";
In the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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use by non-profit institutions as ic
modified and this statement is not rem
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Ol-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2090 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
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hes 153;
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                                                                                                                                                                                                                                                       Lutfalla G., Gardiner K., Uze G.;
"A new member of the cytokine rec
21 at less than 35 kb from IFNAR.
Genomics 16:366-373(1993).
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                                                    This SWISS-PROT entry is copyright. It is produced through a control of the Swiss Institute of Bioinformatics and the EMBL the EUROpean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch). "
EMBL; Z17227; CAA78933.1;
EMBL; U08988; AAA86872.1;
PIR; A47003; A47003.
HSSP; P13726; IDAN.
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MEDLINE; 93300510.
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FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.

SUBJECTLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RI
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31, Last sequence update)
34, Last annotation update)
CLASS-II CRF2-4 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                restrictions
                                                                                                                                           OF RECEPTORS
                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                              IFNAR
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                                                                                                             a collaboration
                                                                                                                                                                                                                                                                                        chromosome
                                                                            for
                                                                                                            outstation
                                                                ch/announce/
                                                                                      in
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RESULT 6
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Best Local S
Matches 66
 This SWISS-PR
between the
the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                   Soh J. Donnelly R.J., Kotenko S.,
Wang N., Emanuel S.L., Schwartz B.,
"Identification and sequence of an
activation of the human interferon
                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                  INGS_HU
P38484;
                                                                                                                                                                                  TISSUE=LUNG FIBROBLAST;
MEDLINE; 94170380.
                                                                                                                                                                                                                                                               RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA IFNGR2 OR IFNGT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                        EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                     176
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                                   1 76:793-802(1994).

FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART THE IFN-GAMMA SIGNAL TRANSDUCTION PARHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.

SUBJECTLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBJECTLULAR COCTAINS: 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                     EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                  HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WVLSAAAGGKNLKS------PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRIFODKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                               Metazoa;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
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20
221
250
66
188
102
102
161
124
124
269
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                                                                                                                                                                                                                                                   (Human).
                                                                                                                                                                                                        N.A.
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                                                                                                                                                                                                                                                                                                                                              STANDARD;
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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 222.5;
Pred. No. 1.36
10; Mismatches
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FLGHP ->
MISSING (
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CYTOPLASMIC (P
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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A -> D (IN
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i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A -> D (IN REF. 2).
FLGHP -> VGRME (IN
MISSING (IN REF. 2)
66706C79F8514B23
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                    S., Mariano T.M., Coo
z B., Miki T., Pestka
f an accessory factor
eron gamma receptor.";
                                                                                                                                                                                                                                                                                                                                              337
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LULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
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.3e-12;
es 93;
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                                                                                                                                                                                                                                                                                      (INTERFERON-GAMMA
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                                                                                                                                               cook J.R.,
stka S.;
stor required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                         Mammalia;
                                            DOMAINS.
LLY OF RECEPTORS
                                                                                                                                                                                                                                                                          TRANSDUCER-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                            INGR_HUMAN
P15260;
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VARIANT
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CARBOHYD
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                                                         Aguet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U05875; AAA16955.1; -.
EMBL; U05877; AAA16956.1; -.
MIM; 147569; -.
                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                            SEQUENCE
                                                                                             Eutheria;
                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                                                                                 Homo sapiens (Human).
                                                                                                                             FNGR1
                                              Molecular cloning
                                                                                                                                                                                                                                     233
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         ESULFIDE
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                                                                                                                                                                                                                                                                                                                GALHSAWVTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
                           55:273-280(1988).
                                                                                                                                                                                                                                     SCYETMAD
                                                                                                                                                                                                                                                         HCIKTTVE
                                                                                                                                                                                                                                                                            YYVHYWE---KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                                                                                                                                                                                                                                                                     ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT
                                                                                                                                                                                                                                                                                                                                                          YTDSK----
                                                                                                                                                                                                                                                                                                                                                                           FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                               LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK 68
                                                                                                                                                                                                                                                                                                                                                                                                                  VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS 62
                                                                                                                                                                                                                                                                                               YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV
                                                        E FROM N.A.
89003065.
Dembic 2
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93183911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement
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                                                                                              Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                        -WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                     STANDARD;
         PARTIAL
                                              and expre
                                                                                              Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37834
                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%;
                                               expression
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         SEQUENCE,
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                                                       a
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Pred.
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
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/FTId=VAR_002718.
18C61B10AD90E509 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                               of.
         AND
                                                                                                                                                                                                                                                                                                                                                                                                                                             151.5; DB 1
No. 2.7e-06;
                                               the
                                                                                                                                                                                     489
                                                                                                                                     update)
PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
         MUTAGENESIS
                                               human interferon-gamma
                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its content
                                                                                                                                     (CDW119)
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                         119
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Ş В Ş

FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA---EKENTSSWYEV MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEY--QIMPQVPV VVLLGATTLVLVAVGPWVLSAA-AGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNV-T Query Match Best Local S Matches 52

Similarity

Score 117.5; DB 1; Pred. No. 0.0045; 4; Mismatches 99;

1;

Length

35;

Gaps 60

8

Conservative

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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                           TRANSMEM
DOMAIN
DISULFID
DISULFID
DISULFID
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                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Neutralizing epitopes on the extracellular interferon gan (IFNgammaR) alpha-chain characterized by homolog scanning and X-ray crystal structure of the A6 fab-IFNgammaR1-108 J. Mol. Biol. 273:882-897(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Crystal structure of a complex between interferon-gamma and soluble high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95342235.
Walter M.R., Windsor W.T.,
Zauodny P.J., Narula S.K.;
                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                     PDB; 1JRH; 25-MAR-98
MIM; 107470; -.
                                                                                                                                                                                                                                                                                                                                                                                     PIR; A31555;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J03143; AAA52731.1; PIR; A31555; A31555.
                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sogabe S., Stuart F., Henke C., Winkler F.K., Robinson J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX MEDLINE; 98035727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 32:2423-2430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gan "Allgament of disulfide bonds of the extracellular domain interferon gamma receptor and investigation of their role biological activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

PTM: PHOSPHORYLATED AT SER/THR RESIDUES.

SIMILARITY: CONTAINS 2 IMMUNOSLOBULIN-LIKE C2-TYPE DOMAINS.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERFERON-GAMMA DIMER.
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                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                         domain;
                                                                54404
9.8%;
                                                                                                                                                                                                                                                                                                         3D-structure
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CYTOPLASMIC (POTENTIAL)
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SEQUENCE OF 1-28 FROM N.A.

(MEDLINE; 95197006.

NEAVAL P., Obicl S., Russell S.W., Murphy W.J.;

"Characterization of the 5' flanking region and gene mouse interferon-gamma receptor.";

Gene 154.219-223(1995).

-i- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECIONSTREED TOTALLED AT SER/THR RESIDUES.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- STMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray P.W., Leong S., Fenn Fernandez-Luna J., Schrei. "Cloning and expression or receptor.";
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                                                                                                                                         Appella E.;
"Affinity purification, peptide analysis,
mouse interferon gamma receptor.";
T. Biol. Chem. 265:4064-4071(1990).
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Mus musculus (Mouse).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Munro S., Maniatis T.; "Expression cloning of Proc. Natl. Acad. Sci.
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Eutheria; Rodentia;
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EMBL; M26711; AAA37896.1; -.
EMBL; M28233; AAA37898.1; -.
EMBL; M25764; AAA39177.1; -.
EMBL; J05265; AAA39178.1; -.
EMBL; U05960; AAA80980.1; -.
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PIR; A36224;
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an email to license@isb-sib.ch)
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nilarity 22.9%;
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A34508.
 (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 37, Last annotation update)
-10 RECEPTOR PRECURSOR (IL-10R).
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"A receptor for interleukin 10 is related to interferon receptors.";

Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).

-I- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Mus musculus (Mouse)
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(Rel. 36, Last annotation updat
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82089CD576F686B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                 95.5;
No. 0.
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            update)
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RESULT 11
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Best Local S
Matches 38
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REPEAT 1
REPEAT 3
REPEAT 4
REPEAT 4
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Caenorhabditis elegans.
TISSUE-LYMPHOMA;
MEDLINE; 94165477.

Liu Y., Wel S.H.-Y., Ho A.S.-Y., de Waal Malefyt R.,
"Expression cloning and characterization of a human:
"Immunol. 155:1821-1829(1994).
-I. Tumunol. 155:1821-1829(1994).
-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                        MYEARA OR ILLUA.
LL10RA OR ILLUA.
HOMO saplens (Human).
Homo saplens (Human).
Homo saplens (Chunan).
Homo saplens (Catarrhini;
                                                                                                                                                                                                                                  I10R_HUMAN
Q13651;
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                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
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PFAM; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORMPEP; F55F8.3; CE11192.
PRINTS; PR00320; GPROTEINBRPT.
                                                                                              SEQUENCE FROM
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mitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: CONTAINS 6 MD REPEATS (TRP-ASP DOMAINS).
SIMILARITY: BELONGS TO THE PWP2 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                  IHEFGKSIENKVYNPFSLSRTYKLSSDS
                                                                                                                                                                                                                                                                                                                                                                     LSISPSGYHLLASDERGVVHFVHLLSEFKIYTFRSNKPIGSLQWSPDATRVAICRENDLQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00678; WD_REPEATS;
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188 218
358 388
400 430
486 514
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Pred. No. 0.91
9; Mismatches
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                                                                                                                                      Mammalia;
               HIGH AFFINITY
                                        receptor.";
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Best Local S
Matches 51
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P30931;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor;
SIGNAL
                              Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovi
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                                                                                                            01-JUL-1993 (Rel.
01-JUL-1993 (Rel.
01-NOV-1997 (Rel.
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                                                                                               TISSUE FACTOR
                           Bovinae;
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                                                                                                                                                                                                                                                                                                                       NSSGVEERIENIYSRHKIYKLSPETT---
                                                                                                                                                                                                                                                                                                                                                   TRFSVDEVT----LTVG--SVNLEIHNGFILGKIQLPRPK-----
                                                                                                                                                                                                                                                                                                                                                                             --YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                              Rel. 35, Last annotation update)
PRECURSOR (TF) (COAGULATION FACTOR
                                                                                                                                                                   STANDARD;
                                                                                                            26, Created)26, Last sequence update)35, Last annotation updat
 AND
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19.7%;
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 PARTIAL SEQUENCE
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POTENTIAL.
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                                                                                                                                                                     PRT;
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                                          Bovidae;
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RESULT 1
TF_HUMAN
ID TF_H
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DT 01-J
DT 115-J
DT 115-J
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OS HOMOO
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CARBOHYD
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DISULFID
DISULFID
LIPID
                                                                                            TF_HUMAN STANDARD; PRT; 295 AA. P13726; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR (THROMBOPLASTIN) (CD142 ANTIGEN).
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"CDNA and amino acid sequences of bovine tissue factor.";

Biochem. Biophys. Res. Commun. 181:1145-1150(1991).

-I- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGACION OF THE COAGULATION PROTEASE CASCADE.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00346; TISSUEFACTOR, PROSITE; PS00621; TISSUE_FACTOR; PFAM; PF01108; Tissue_fac; 1.
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                                                   Homo sapiens (Human)
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: || :|:|: : || || :|: :||
LGNW--KNKCFYTTNTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WK-NSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
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  Primates;
                            Metazoa;
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  Chordata; Craniata; Ve Catarrhini; Hominidae;
                            Chordata;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 89247359;
Mackman N., Morrissey J.H., Fowler
"Complete sequence of the human ti
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                                                                                                                                                        WEDLINE; 96190957.

Wuller Y.A., Ultsch M.H., de Vos A.M.;

"The crystal structure of the extracellular factor refined to 1.7-A resolution.";

J. Mol. Biol. 256:144-159(1996).
                             MEDLINE;
Bach R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrissey J.H., Fakhrai H., Edgington T.S.; "Molecular cloning of the cDNA for tissue factor, the receptor for the initiation of the coagulation proteas (c) 50:129-135(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.; "Isolation of cDNA clones coding for human tissue factor: structure of the protein and cDNA."; proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
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                                                                                                                                                                                                                                               wuller Y.A., Ultsch M.H., Kelley R.F., "Structure of the extracellular domain location of the factor VIIa binding sit piochemistry 33:10864-10870(1994).
                                                                                                                                                                                                                                                                                                                            "Human tissue factor contains thioester-linked on the cytoplasmic half-cystine."; Biochemistry 27:4227-4231(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the gene."
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                                                                                                                                                                                                                          (-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
 PROPAGATION OF THE COAGULATION PROTEASE CASCADE. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPO
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87244317.
                                                                                                                                                                                                                                                                                                                                                                                                          .L., Gorman C.M., Vehar G.A., O' and expression of human tissue Res. 48:89-99(1987).
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of human tis
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EMBL; M16553; F
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EMBL; A19048; C
EMBL; A19048; C
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PIR; A43645; A4
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PFAM; PF01108; Tis
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PROSITE;
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                                                                EPLYENSPETTYLETNIGOPTIOSFEQVGTKVNVTVEDERTLVR-
                       VFGKDLIYTLYYWKSSSS-GKKTAKTNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTD
                                            --GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL--LTSWKIGVY
                                                                                                             ----TKSGDW--KSKCFYTTDTECDLTD----EIVKDVKQTYLARVFSYPAGNVESTGSAG
                                                                                                                                                                                                      52;
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                                                                                       WYEVDSFTPFRKAQIGPP-----
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                                                                                                                                                          -GWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQIS-
                                                                                                                                                                                                                7.78;
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42;

EVHLEAEDKAIVIHISPGTKDSVMWALD-

160

122 114 72

RNNTFLSLRD

177

Score 92; DB Pred. No. 0.44 42; Mismatches

DB 1;

Length 295 Indels

52;

Gaps

13;

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use by non-profit institutions as long a modified and this statement is not removed.
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A43645; A43645.

A47574.

1BOY; 10-JUN-96.

2HFT; 29-JAN-96.

1DAN; 04-SEP-97.

1TFH; 25-FEB-98.

1AHW; 19-AUG-98.
                                                                                                                                                                                                                                                                                                                                                                                                                               RESPONSE.
DATABASE: NAME-PROW; NOTE-CD guide CD142 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd142.htm".
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                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a centry the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict European Bioinformatics institute. There are no restrict by non-profit institutions as long as its content is
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                                                                                                                                                                                          PR00346; TISSUEFACTOR
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                                                                                                                                                                                                                                                                                                 AAA61150.1;
AAA61151.1;
AAA61152.1;
AAA36734.1;
CAA01438.1;
                                                                                                                                                            Blood coagulation;
                                                                                                                                                 structure.
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  MW;
                                                                    WKS MOTIF.
  PALMITATE.
V -> A (IN REF. 4).
D3486C713ED8EADO CRC64;
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CYTOPLASMIC (POTENTIAL)
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SPVECM

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TISSUE-LYMPHOCYTES;

MEDLINE; 88061067.

Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;

Tifferential usage of three exons generates at least five mRNAs encoding human leukocyte common antigens.";

J. Exp. Med. 166:1548-1566(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LEUKOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.3.48)
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P08575;
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                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streuli M., Krueger N.X., Thai T., Tang "Distinct functional roles of the two idomains of the receptor-linked protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charbonneau H., Tonks N.K., Walsh K.A., Fischer E "The leukocyte common antigen (CD45): a putative protein tyrosine phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
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Charbonneau H., Tonks N.K.,
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PTPRC OR CD45.
              PFAM; PF00041; fn3; 2.
PFAM; PF00102; Y_phosphatase; 2.
Glycoprotein; Transmembrane; Phosphorylation;
                                                                    PRINTS; PRO0700; PRTYPHPHTASE.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 2.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
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Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF L-CA,
WHICH ARISE BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD45 entry;
WMW-"http://www.ncbi.nlm.nih.gov/prow/cd4/cd45 htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) J. 9:2399-2407(1990).
FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN FRECEPTOR. THE FIRST PYPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE RECEPTOR. ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPEC
THE FIRST ONE.
CATALUTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE +
PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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splicing; Hydrolase;
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Signal
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two intracellular phosphatase like
tein tyrosine phosphatases LCA and
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Best Local :
                                                                                                                                                                                                                                                P26690;

Ol-AUG-1992 (Rel. 23, Created)
Ol-AUG-1992 (Rel. 23, Last sequence update)
Ol-AUG-1992 (Rel. 23, Last sequence update)
Ol-AUG-1992 (Rel. 23, Last annotation update)
Ol-AUG-1992 (Rel. 23, Last annotation update)
Ol-AUG-1992 (Rel. 23, Last annotation update)
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CHAIN
              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN-CV. HAROSOY 63;

MEDLINE; 91177016.

Welle R., Schroeder G., Schiltz E., Grisebach H., Schroeder C., Indiced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63)

phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63)

phytoalexins in 196:423-430(1991).

FUNCTION: CO-ACTS WITH CHALCOME SYNTHASE IN FORMATION OF 12.2, 4.-TRIHYDROXXCHALCOME. INVOLVED IN THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOYBN
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Pred. No. 3.9;
23; Mismatches
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FIBRONECTIN TYPE-III (POTENTIAL).
PROTEIN-TYROSINE PHOSPHATASE.
PROTEIN-TYROSINE PHOSPHATASE.
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W; 1F357BC5632618B2 CRC64;
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Search completed: June
Job time: 14317 sec
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Best Local Similarity
Matches 49; Conserv
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PIIR; S14222; S14222.
HSSP; P14550; ZALR.
PRINTS; PRO0069; ALDOKETRDTASE.
PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
PFAM; PF00248; Aldo_ket_red; 1.
Flavonoid biosynthesis; Oxidoreductase; NADP.
SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- INDUCTION: BY PATHOGEN ATTACK.
-i- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - 1 - SUBUNIT: MONOMER.
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                                                                                                                                                                                              218
                                                                                                           265
                                                                                                                               173 SSGVEERIENIY------SRHKIYKLSPETTYCLKVKAALLISW 210
                                                                                                                                                                                                                                                                                                                                                              105 KSLKTLQLEYLDL----YLIHWPLSSQP-GKFSFPIEVEDLLPFDVKGV--WESMEECQK 157
                                                                                                                                                                                                                                  123 FRK-AQIGPPEVH------LEAEDKAIVIHISPGTKDSVMWALD-GLSFTYSLLIWKN 172
                                                                                                                                                                                                                                                                             158 LGLTKAIGVSNFSVKKLQNLLSVATIRPVVDQVEMNLAWQQKKLREFCKENGIIVTAFSP 217
                                                                                                                                                                                                                                                                                                                        28 KNIKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFD-----YOKTGMDNWIKLSGCON 81
                                                                                                     SYDKERMNQNLHIFDWALTEQDHHKISQISQSRLISGPTKPQLADLW 311
                                                                                                                                                                                        LRKGASRGPNEVMENDVLKEIAEAHGKSI-----AQVSLRWLYEQGVTFV-----PK 264
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                 1, 2000, 04:38:54
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Title:
Perfect score:
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Maximum DB
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Listing first 45
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Match
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
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sp_unclassified:*
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sp_virus:*
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088307
015467
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Q61190
Q63953
Q9YGC8
Q14936
Q23020
Q23550
Q23551
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                  028733 oryctolagus

016614 homo sapien

099hv9 gallus gall

054711 mus musculu

095209 oryctolagus

088307 mus musculu

015467 homo sapien

012465 saccharomyc

099624 homo sapien

p97378 mus musculu
                                                                                                                      Q9yhw0 gallus gall
Q61190 mus musculu
Q6395 mus musculu
Q6395 mus musculu
Q9ygc8 gallus gall
Q14936 homo sapien
Q23020 caenorhabdi
Q23550 caenorhabdi
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26926 429 2214 430 406 7466 7465 508 817 1093 11040 11093 11493 11493 11526 962 962 952 952 952 952 952 952 952 952 952 95
3 3 4 4 10 110 110 110 110 110 110 110 110
Q10466 Q106103 Q92673 Q23854 Q23854 Q58459 Q59459 Q70734 Q20993 Q70735 Q58863 Q94537 P9779 Q94537 P9779 Q94537 P9779 Q94537 P9779 Q94537 Q94538 Q9453
Q10466 homo sapien Q06103 saccharomyc Q92673 homo sapien Q23854 brassica ca Q58459 methanococc Q90754 foot-and-mo Q20930 caenorhabdi Q07784 gallus gall Q0778535 rattus norv Q9w675 brachydanio Q5863 methanococc Q94537 drosophila P97798 mus musculu Q94538 drosophila Q60705 mus musculu Q70367 rattus norv Q94977 homo sapien Q35664 mus musculu Q35664 mus musculu Q35663 mus musculu Q35863 mus musculu

## ALIGNMENTS

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179 RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224 :: :     :           :     ::  :      186 KVRSILPIDVINDLAPETTYCLKVQATVPLEDKGGLFSPIHCIKTT 231	121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEE 178  :          : :      :   :       :     : :	67KTGMDNWIKLSGCONITSTKCNESSLKLNVYEEIKLRIRAE-KENTSSWYEVDSF 120	7 GATTLVLYAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ 66 	Query Match 36.0%; Score 430.5; DB 13; Length 569; Best Local Similarity 43.8%; Fred. No. 7.4e-31; Matches 99; Conservative 37; Mismatches 79; Indels 11; Gaps 6;	Receptor. SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;	receptor gene cluster.; Genome Res. 0:0-0(1999) EMBL; AF082664; AAD13669.1;	SEQUENCE FROM N.A. TISSUE-LIVER; REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.; "Comparative genomic analysis of the interferon/interleukin-10	Gallus gallus (Chicken). Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. []]	01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) INTERFERON ALPHA/BETA RECEPTOR 1.	LT 1 WO WOYHWO PRELIMINARY; PRT; 569 AA.

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Best Local Similarity
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063953; OTTEMBLEEL. 01, Created)
01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-NOV-1996 (TIEMBLEEL. 12, Last annotation update)
01-NOV-1999 (TIEMBLEEL. 12, Last annotation update)
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Gene 186:97-101(1997).

EMBL; U53696; AAC53062.1;

MGD; MGI:109380; I110rb.

PFAM; PF00041; fn3; 1.
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MIS musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Ver

Eukaryota: Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            061190:
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
ILIORB OR CRFB4 OR CRF2-4.
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE: 94170381.
HEMMI S., BOHNI R., STARK G., DI MARCO F.,
"A novel member of the interferon receptor
functionality of the murine interferon gamm
cells.";
                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Rodentia; Sciurognathi; Muridae;
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                        SEQUENCE FROM N.A.
STRAIN-129SV/J;
MEDLINE; 97128072.
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                                                                                                                  Cell 76:803-810(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 VHLEAEDKAIVIHIS------PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 VGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CKRTASTQCDFS--HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGFLLVPALG--MIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 AA;
c.,
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  RHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of cDNA
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28.2%;
  s;
MUTHUKUMARAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 219; DB 11;
Pred. No. 4.5e-12;
7; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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ae; Murinae;
                                                                                                                                                                                                                                                                                                                            Vertebrata;
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  LEMBO
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Mus.
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Mus.
  DONNELLY R.,
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Best Local S
Matches 69
                                                                                                                                                                                 Query Match
Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                             REBOUL J., GARDINER K., MONNERO "Comparative genomic analysis o receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082666; AAD13678.1; -.
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O9YGC8;
O1-MAY-1999 (TrEMBLrel 10, C
O1-MAY-1999 (TREMBLrel 10, I
O1-MAY-1999 (TREMBLrel 10, I
INTERLEUKIN-10 RECEPTOR 2.
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                                                                                                                                                                                                                                                                                                      Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL10R2.
Gallus (Chicken).
Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Archosauria, Aves;
Neognathae: Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:107654; Ifr
I; PF00041; fn3;
ENCE 332 AA;
                                                                                                                  PQKVEVDIIDDNFILRWNRSDESVGNVTFSFD----YQKTGMDNWIKLSGCQNITSTKCN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
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VSS--LSVYGAYVLRVRTEWEDEHSDWAVVRFKPMADTVIGPPSVNVKSESGTLHVDFTG
                                         FSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS- 148
                                                                                          PRNARISSVNFRSVLLWDPPGVRKGNLSYTVQAKSIFPKQNFNN----VTTNLNVTECD
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                                                                                                                                                                                                                                                                                                      341 AA;
                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                      39062 MW;
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Last annotation updat
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Pred. No. 1.2e
88; Mismatches
                                                                                                                                                                                                       Score 179;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                      7433D364 CRC32;
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interferon/interleukin-10
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                                                                                                                                                                                 DB 13;
.8e-08;
les 84;
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.2e-10;
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                                                                                                                                                                                                                                Length 341;
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EMBL; U19241; AAC52064.1; JOINED.
EMBL; U19243; AAC52064.1; JOINED.
EMBL; U19244; AAC52064.1; JOINED.
EMBL; U19244; AAC52064.1; JOINED.
EMBL; U19245; AAC52064.1; JOINED.
EMBL; U19246; AAC52064.1; JOINED.
EMBL; U19246; AAC52064.1; JOINED.
SEQUENCE 484 AA; 53818 MW; EBCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q14936 PRELIMINARY; PRT; 484 AA. Q14936; Q14936; O1-NOV-1996 (TIEMBLIEL 01, Last sequence update) 01-NOV-1996 (TIEMBLIEL 08, Last annotation update) 01-NOV-1998 (TIEMBLIEL 08, Last annotation update) INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 97246734.
MERLIN G., VAN DER LEEDE B.-J.M., MCKUNE K., KI
BANNWARTH W., ROMQUIN N., VIEGAS-PEQUIGNOT E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 89003065.
AGUET M., DEMBIC 2.,
"Molecular cloning a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    "The gene for receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 45:413-421(1997).
                                            157
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                                                                                                                                                                                     VQ-GVIPEWNKTGERSQELCEQTT
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                                                                                                                                                                          MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEY--QIMPQVPV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55:273-280(1988).
                                                                 ERIENIYSRHKIYKLSPETTYCLKV
                                                                                       EEFAVCRDGKIGPPKLDIRKEEKQIMIDI - - -
                                                                                                         DSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                              FTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKE--SAYAKS 116
                                                                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA---EKENTSSWYEV 117
                                                                                                                                                                                                                    9.5%;
llarity 22.9%;
Conservative 4
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                                            YDPETTCYIRV
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                                                                                                                                                                                                                   Score 113.5; DB Pred. No. 0.022; Mismatches
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Best Local S
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Q23020;
Q23020;
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Q23020;
Q1-NOV-1996 (TIEMBLICEL: 0:
Q1-NOV-1999 (TIEMBLICEL: 1:
Q1-NOV-1999 (TIEMBLICEL: 1:
                                Q23550
Q23550;
Q1-NQV-1996
Q1-NQV-1998
Q1-NQV-1999
           UNC-22
UNC-22.
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STRAIN-BRISTOL N2;
MEDLINE; 90044042.
BENIAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G.,
"Sequence of an unusually large protein implicated in
myosin activity in C. elegans.";
Nature 342:45-50(1989).
[2]
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BENIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
"Additional sequence complexity in the muscle
encoded protein, twitchin, of Caenorhabditis e
Genetics 134:1097-1104(1993).
Caenorhabditis elegans
                                                                                                                                1211
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MEDLINE; 93387664.
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                                                                                                                                VIEKKGKHGRDWQ 1223
                                                                                                                                                     CLKVKAALLTSWK 211
                                                                                                                                                                                                                     KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                   TSTKCNFSSLKLNYYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA
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                    N-1996 (TrEMBLrel. 01, (
NV-1998 (TrEMBLrel. 08, 1
NV-1999 (TrEMBLrel. 12, 1
2 PROTEIN.
                                                                                                                                                                                                IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                          8.2%; Score 97.5; I flarity 22.8%; Pred. No. 17; Conservative 22; Mismatches
                                                                                                                                                                          -GTPDVVDWDADRVS----
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annotation updat
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elegans.";
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EMBL; 273899; CAA98064.1; JOINED.
HSSP; P02751; IFAN.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 19; 17.
PFAM; PF00069; pkinase; 1.
PRINTS; PR00011; FNTYPEIII.
SEQUENCE 6831 AA; 752579 MW; 0
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HANKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUUDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., MATERSTON R.,
                                                                                                                     WATSON A., WEINSTOCK L., WILKINSO "2.2 Mb of contiguous nucleotide elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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SEQUENCE FROM N.A. WHITE S.;
Submitted (MAY-199
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Eukaryota; Metazoa; Nen
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EMBL; 273897; CAA9800
                                                                           Nature 368:32-38(1994).
[3]
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Best Local
                                                                                                                                                                                              MEDLINE; 90238553.

LABEIT S., BARLOW D.P., G
FRANCKE U., LEONARD K., W
"A regular pattern of two
of titin.";
                                                          EMBL; X64696; CAA45937.1;
EMBL; X17329; CAA35207.1;
HSSP; P56276; lTLK.
PFAM; PF00041; fn3; 50.
PFAM; PF00047; 1g; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITIN (FRAGMENT).
OryCtolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seg
01-NOV-1999 (TrEMBLrel. 12, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2185
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PFAM;
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EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92258380.
LABEIT S., GAUTEL M., LAKEY A.,
"Towards a molecular understand
EMBO J. 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CE12;
LABEIT S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q28733 PRE
Q28733; Q28736;
                                                                                                                                                                           Nature
                                                                                                                                                                                                                                                                                                          TISSUE-PSOAS MUSCLE;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4305-5320 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CE12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-6805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
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273897; CAA98065.1; JOI

273899; CAA98065.1; JOI

273899; CAA98065.1; JOI

273899; CAA98065.1; JOI

273899; CAA98065.1; JOI

274, PF00047; fn3; 31.

275; PR00047; ig; 17.

275; PR00091; FNTYPEIII.

2760 AA; 789211 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIEKKGKHGRDWQ 2335
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44; Conserv
                                                                                                                                                                         345:273-276(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                  understanding
                                                                                                                                                                                                                   two types
                                                                                                                                                                                                                   GAUTEL M., GIBSON T., WARDALE J., WHITING A. wo types of 100-residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                    cx J.;
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                                                                                                                                                                                                                                           HOLT J., HSIEH C.L., ., TRINICK J.;
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Best Local
EMBL M23461 FEMBL M23466 FEMBL M23466 FEMBL M23469 FEMBL M23470 FEMBL M23471 FEMBL M23473 FEMBL M23474 FEMBL M23475 FEMBL M23476 FEMBL M23477 FEMBL M23477 FEMBL M23477 FEMBL M23478 FEMBL M23478 FEMBL M23478 FEMBL M23478 FEMBL M23478 FEMBL M23478 FEMBL M23479 FEMBL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q16614;
Q16614;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euraryota; Metazoa; Chordata; Hominidae; Homo.
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EMBO J. 6:1251-1257(1987).
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MEDLINE; 87275816.
RALPH S.J., THOMAS M.L., MORTON C.C
"Structural variants of human T200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.NOV-1996 (TIEMBLrel. 01, Created)
01.NOV-1996 (TIEMBLrel. 01, Last sequence update)
01.NOV-1999 (TIEMBLrel. 12, Last annotation update)
T200_LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR
                                                                                                                                                                                                                                                    EMBL; M23492; AAD15273.
                                                                                                                                                                                                                                                                 "Complete exon-intron organizati
antigen (CD45) gene.";
J. Immunol. 141:2781-2787(1988).
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                                                                                                                                                                                                                                                                                                                  HALL L.R., STREULI M.,
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                MEDLINE; 89009812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E----NTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI-------HISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGMDNWIKLSGC -- QNITSTKCNFSSLKLNVY -------EEIKLRIRAEK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54:
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54; Conservative
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                                                                                                                                                                                    AAD15273.1;
AAD15273.1;
AAD15273.1;
AAD15273.1;
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21.78;
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                                                                                                                                                                                                                                                                                                organization
                                                                                                                                                                                                                                                                                                 SCHLOSSMAN S.F., SAITO H.; preparation of the human leukocyte common
                                                                                                                                                                                                                                                                                                                                                                                                                                          MORTON C.C.,
                              JOINED
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Best Local S
Matches 36
                                                                          Query Match
Best Local
                                                             Matches
                                                                                                                                                                                                                                                                                                                                                               Q9YHV9;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MOV-1999 (TrEMBLrel. 12, Last annotation update)
INTERFERON ALPHA/BETA RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
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EMBL;
EMBL;
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                                                                                                                                                                    Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1;
HSSP; P13726; 1TFH.
                                                                                                                                                                                                                  REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of receptor gene cluster.";
                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata;
Neognathae; Galliformes; Phasianidae; Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6AHX6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00041; fn3; 2.
PFAM; PF00102; Y_phosphatase;
PRINTS; PR00700; PRTYPHPHTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P18052;
                                                                                                                                                                                                                                                                 ISSUE=LIVER;
                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 KNIETFTCDTQNITYRFQCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 DESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
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                           2 MVVLLGAT----TLVLVAVGPWVLSAAAGGKNLKSPQKV--EVDIIDDNF--ILRWN-RS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDSVMWALDGLSFTYSL----LIWKNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKW 162
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M23481
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 METLMGGPLRFYQLVFVSI----LCAACYSSLSEKIPREPPDNLQMTSNNFQHILSWRAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGT------ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEKYANITVDYLYNK-----
                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00700; PRTYPHPHTASE.
Alternative splicing; Hydrolase.
1 23 POTENTIAL.
                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 11
1143 AA;
                                                                                                                                        508 AA;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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AAD15273.
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AAD15273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%;
                                                                                                                                        57049 MW;
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                                                                          7.5%;
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                                                             35;
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; Pred. No. 8.2;
23; Mismatches
                                                          Score 89.5; DB Pred. No. 3.5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                          2DC4E498 CRC32;
                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                    UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 AA
                                                                                                                                                                                                                                                                                                             Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                               Vertebrata;
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                                                                                           В
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60;

Indels

53;

Gaps

6,

198

Length 1143;

13; 96;

508;

Archosauria;

Indels Length

71;

Gaps

15;

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RESULT
O54711
ID AC O54711
DT O5
DT 
    RESULT
Q95209
ID Q0
AC Q0
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DT 00
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Best Local S
Matches 33
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SUESENS U., FENGER U., HERBARTH B
Mech. Dev. 0:0-0(1997).
EMBL; AF031816; AAC16739.1; -.
HSSP; P01130; 1AJJ.
MGD; MGI:1202296; SOr11.
  Q95209;
Q95209;
Q1-FEB-1997
Q1-FEB-1997
Q1-NOV-1999
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054711;
                                                                                                                                                                                                                                                                                                                                                                                                 1474
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 12, Last annotation update)
SORTILIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00041; fn3; 4.
PFAM; PF00057; ldl_recept_a;
PFAM; PF00058; ldl_recept_b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1202296; Sorll.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GP250) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          44 NFILRWNRSDESV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNKHSIPSAWK-----CITT 233
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                                                                                                                                                                                                            GDIKVN-GYVVNLFWSFDAHKQEKKTLSFRGGSALSHKVSNL-TAHTSYEIS
                                                                                                                                                                                                                                                     --IHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                   NLLLNALYTVRV-AAVTSRGIGNWSDSKSITTIKGKVIQAPNIHIDSYDENSLSFTLTMD
                                                                                                                                                                                                                                                                                                                                                                                              NLQLSLNREEEGVILGHWAPPVHTHGLIREYIVEYSRSGSKMWASQRAASNSTEIK----
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  7 (TrEMBLrel.
7 (TrEMBLrel.
9 (TrEMBLrel.
                                                                                             PRELIMINARY;
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19.2%;
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Created)
Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; DB Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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update)
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                                                                                                                                                                                                                                                       193
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                                                                                                                 KANAKI T., BUJO H., HIRAYAMA S., TANI
MORISAKI N., SCHNEIDER W.J., SAITO Y
"Developmental regulation of LR11 ext
DNA Cell Biol. 0:0-0(1998).
EMBL; AB015790; BAA31219.1; -.
HSSP; P01130; 1AJJ.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01209; LDLRA_1; 10.
PFAM; PF00057; ldl_recept_a; 11.
PFAM; PF00058; ldl_recept_b; 4.
PFAM; PF00041; fn3; 5.
PRINTS; PR00261; LDLRECEPTOR.
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. Biol. Chem. 271:24761-24768(1996).
EMBL; D86350; BAA13075.1; -.
HSSP; P01130; laJJ.
PROSITE: PS11209; LDLRA_1; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          088307;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1809
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96394640.
YAMAZAKI H., BUJO H., KUSUNOKI J., SEIN SCHMEIDER W.J., SAITO Y.;
"Elements of neural adhesion molecules
                      PFAM; PF00057; ldl_recept_a; PFAM; PF00058; ldl_recept_b; PFAM; PF00041; fn3; 4. PRINTS; PR00261; LDLRECEPTOR
                                                                                                                                                                                                                                                                                         TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          088307
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32; Conserv
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     LDLRECEPTOR FNTYPEIII.
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Last sequence update)
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                          Query Match 7.4%; Score 89; DB 4; Length 239; Best Local Similarity 22.7%; Pred. No. 1.4; Matches 46; Conservative 26; Mismatches 83; Indels
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SEQUENCE 2215 AA; 247021 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-BLOOD;
MEDLINE; 95279874.
NOVICK D., COHEN B., TAL N., RUBINSTEIN M.;
NOVICK D., COHEN B., TAL N., RUBINSTEIN M.;
"Soluble and membrane-anchored forms of the human IFN-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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J. Leukoc. Biol. 57:712-718(1995).
-i- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
EMBL; X89814; CAA61940.1; -.
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SIGNAL 1
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                                    198
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206 YCVSVYLEHSDEQAV-IKSPLKC 227
                                                                                                                                              107 VTVLEGFSGNTTLFSCSHNFWLAIDMSFE------PPEFEIVGFTNHINVMVKFPSIV 158
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                                   YCLKVKAALLTSWKIGVYSPVHC 220
                                                                                                     DSVMWALDGLSFTYSLLIWKNSSGVEERIENTYSRHK-----IKLSPETT 197
                                                                      E-----EELQFDLSLVI------EEQSEGIVKKHKPEIKGNMSGNFTYIIDKLIPNTN 205
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                                                                                                                                                                                                                                                                                                                                                                                     27 239 SOLUBLE IFN ALPHA/BETA RECEPTOR BETA CHAIN.
239 AA; 27336 MW; 9DA1F03E CRC32;
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239
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Primates; Catarrhini; Hominidae; Homo.
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PVFNIRSLSDSFHIYIGAPKOSGNTPVIODYPLIYEIIFWENTSNAERKIIEKKTDVT
VPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGNTSK*
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cocation/Qualifiers
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1343 bp 1 Interferon receptor ge A32389.1 GI:1567382

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Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.

Mammalia;

Eutheria;

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Benoit, P. and Meyer, F.
MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECURRALIZING ACTIVITY AGAINST TYPE I INTERFERON PATENT: WO 9320187-A 14-OCT-1993;
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)
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PVFNIRSLSDSFHIYIGAPKQSCNTPVIQDYPLIYEIIFWENTSKAERKIIEKKTDVT
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Primates; Catarrhini; Hominidae;
1 (bases 1 to 1755)
                                                                                                                                                        Patent:
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                                                                                                                                                 FR 2657881-A 20 09-AUG-1991;
Location/Qualifiers
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27. .1700
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/db_xref="GI:1567385"
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                                                                                                   /gene="chimeric IFNalpha/beta-receptor"
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Benoit, P. and Meyer, F.
MONOCLOALA ANTIBODIES AGAINST THE INTERFERON RECEPTOR,
NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON
Patent: WO 9320187-A 14-CCT-1993;
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)
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from Patent
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100.0%; Pr.
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1 (bases 1 to 2755)
Uze,G., Luttalla,G. and Gresser,I.
Genetic transfer of a functional human interferon allinto mouse cells: cloning and expression of its cDNA cell 60 (2), 225-234 (1990)
90124632
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/protein_id="AAA52730.1"
/db_xref="GIB:GO0-120-078"
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HCIKTTVENELPPPENIEVSVONQNYVLKWDYTYANMTFOVQWLHAFLKRNPGNHLYK
WKOJIPDCENVKTTGCVFPQNVFOKGIYLLRVQASDGNNYEWSEBIKFDTEIQAFFLP
PVFNIRSLSDSFHIYIGAPKQSGNTPVIDDYPLIYEIIFWENTSNAERKIIEKKTDVT
VPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVGEKTKFGNTSKULIVGICIALFAL
PFVIYAAKVFLRCINYVFFPSLKPSSSIDEYFSEQPLKNLSTSEEQIEKCFIIENI
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/note="interferon-alpha
1553 c 578 g 79
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79. .159
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putative"
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/db_xref="taxon:9606"
/map="21922.1"
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/note="interferon-alpha receptor
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/map="21" 1750. 1924 1750. 1771

/organism="Homo sapiens" /db\_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                               Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2755)
Myers,R.M.
Unpublished (1996)
                                                                                                                                                                                                                                                                                         Primer A: TGACCAGAAATGAACTGTGTCA
Primer B: TTTAAATAGTTAAGAGCTTGCCCG
STS size: 175
PCR Profile:
Prepared with primer pairs provided by Sandoz,
-- Washington University/Merck EST sequence.
Location/Qualifiers
1. 2755
                                                                                                           Buffer:
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                                                                                                                                                                                                                                                                                                                                                     Email: myers@shgc.stanford.edu
                                                                     MgCl2:
KC1:
Tris-HC1:
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Total Vol:
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     TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
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-	AAATACCTCTAAA 1334               AAATACCTCTAAA 1386	1321 G#        1373 G#	p 64
	ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG 1320 	1261 AT        1313 AT	g dy
<del></del>	AGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACA	1201 CA    1253 CA	pb oy
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	TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140 	1081 CT	ру
	TTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTC	1021 TAC     1073 TAC	D Q
	AAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020 	961 GA    1013 GA	pb oy
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	CAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA 840 	781 ATG	Db
	AGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780 	721 C# 	Db Oy
	TIGGIGICIATAGICCAGIACATIGIATAAAGACCACAGIIGAAAAIGAACIACCICCAC 720 	661 TI    713 TI	D Qy
	 TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 660 	601 TC 653 TC	Оу
	ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC 600 	541 AC     593 AC	g Qy
	GTGTTATGTGGGCTTTGGAT 	481 ATA     533 ATA	D Qy
	GTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAG 480 	421 AA      473 AA	Db
	CATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG 420 	361 CTT     413 CTT	ру
		353 TCAA	₽ .

RESULT 10

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Qy 661 TIGGTGTCTATAGTCCAGTACATIGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC 720	Db 593 ACTCTTCAGGTGTAGAAGAATAGGATTGAAAATATTATTCCAGACATAAAATTTATTAAAC 652  Oy 601 TCTCAGCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 660	Oy 481 ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTATCTGGAAAA 540	Db 413 CTTCATGGTATGAGGTTGACCTATTACACCATTTCGCAAAAGCTCAGATTGGTCCTCCAG 472  Qy 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGGTGATACACAATCTCTCCTGGAACAAAAG 480  Qy 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACAATCTCTCCTGGAACAAAAG 532  Db 473 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG 532	301 TCAAGCTGAATGTTATGAAGAAATTAAATTGCGTATAAGAGAAAAAGAAAAGAAAACACTT	2 2 2 3 8	Qy 61 TGCTCGTCGCCGTGGGCCCATGGGTGTTTCCCGCAGCCGCAGGTGGAAAAATCTAAAAT 120	tches 1332; Conservative 0; Mismatches 2  1 CTGCAGGGATCTGCGGGGGCTCCCAGATGATGGTCGTCCTCC	SION 193602  ON 193602.1 GI:3938072  RDS  Unknown.  E Unknown.  ENCE 1 (bases 1 to 2784)  HORS Mogensen, K. Erik, Uze, G., Lutfall  ENCE 1 (bases)  FONA fragment coding the alpha  for the preparation of a corresp  RNAL Patent: US 5731169-A 1 24-MAR-19  RNAL Patent: US 5731169-A 1 24-MAR-19  RRES  SOURCE /organism="unknown"  COUNT 896 a 553 c 578 g  N  COUNT 896 a 553 c 578 g  Local Similarity 99.9%; Pred. No.	

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VERSION
KEYWORDS
SOURCE
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BTIFNAR
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                                                                                               Submitted (14-SEP-1992) G. Lutfalla, CNRS Lab of Viral Oncology-IRSC, 7 Rue Guy Moquet BP 8, 94801 Villejuif Cedex, 2 (bases 1 to 3230)

Mouchel-Vielh,E., Lutfalla,G., Mogensen,K.E. and Uze,G. Specific antiviral activities of the human alpha interferons determined at the level of receptor (IFNAR) structure FEBS Lett. 313 (3), 255-259 (1992)
                                                                                                                                                                                                                                                                                                                                 BTIFNAR 3230 bp
B.taurus IFNAR mRNA
X68443
                                                                                                                                                                                                                                                                          Bos taurus.
                                                                                                                                                                                                                                                                                                     cytokine receptor; interferon
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Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae;
                                                                                                                                                                                                                   Lutfalla,G.
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                                                                     Location/Qualifiers
 /germline
/tissue_type="kidney"
                            /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                        TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT----CCTGGAACAAAAGATAG
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              TGTTTTTGAAAAATTGAATTGCGCATAAGAGCAGAAGAAGAAACAACACTTCCACATG
951
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197. 1804
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2171. 3230
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643 c 751 g
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ed. No. 5.9e-178;
Mismatches 258;
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                      L06320.1 GI:163187
L06320.1 GI:163187
alpha-interferon receptor.
Bos taurus lung cDNA to mRNA.
Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
 1 (bases 1 to 3284)
Lim, J.K. and Langer,
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and Langer, J.A.
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                                              TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT---CCTGGAACAAAAGATAG
                                                                                    TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAA---CACTTCTTCATG
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GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACA
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KWNSSSESVKNVTESADYQILGTDNWKKLSGCQHITSTKCNFSSVELERVFEKIELRI
RAEEGUNTSTWYEVEPFVPFLEAQIGPDVHLEAEDKAIILSISPGTKDSIMWAMDR
SSFRYSYVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAELRLOSRVGCYSPV
YCINTTERHKVPSPENIQINADNQIYVLKWDYPYENATFQAQWLRAFFKKIPGNHSDK
WKQIPKCENVTSTHCVFPREVSSRGIYYVRVRASNGNGTSFWSEKEFFWENKTIIF
PVISVKSVTDDSLHVSVGAEALIENDRRNKGSSVSDTVCEKTYFENTSNAEKKVLEKRTNF
IFPDLKPLTVYCVKARALIENDRRNKGSSVSDTVCEKTYFGNTSKTWLIVGTCTALFS
IPVVIYVYSVFLRCVKYVFFPSSKPPSSVDEXFSDQPLRNLLLSTSEBQTERFIIEN
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/protein_id="AAA02571.1"
/db_xref="GI:163188"
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/db_xref="taxon:9913"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi Caprinae; Ovis.
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                   TTTAGAAGCTGAAGATAAGGCGATAATACTGAGCATCTCTCCCCCTGGAACAGAAGATAG
                                  TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT---CCTGGAACAAAAGATAG
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158 ASRC, East Campus Drive, Columbia, MO 65211-0001, USA
On Nov 12, 1997 this sequence version replaced gi:1553001
Location/Qualifiers
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Endocrinology 138 (11), 4757-4767
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Han, C.S., Mathialagan, N.,
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/db_xref-"taxon:9940"
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                                          TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAA----CACTTCTTCATG
                                                                                                                                                CAGGAATGTGACTTTTTCAGCAGATTATCAAATACTAGGGACGGATAACTGGAAAAAATT
                                                                                                                                                                TGAGATCCACATCATTGATGACAATTTCTTCCTGAAGTGGAACAGCAGCAGTGAGTCTGT
                                                                                                                                                                                                                        AGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGT
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                             TGTTTTTGAAAAATTGAATTGCGCATAAGAGCAGAAGAAGGAAACAACACTTCTACATG
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97135690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 2559)
Kaluz, S., Fisher, P.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLSLIGATTLMLVAGRWYLPAASGEANLKSENVEIHIIDDNFFL
KWNSSSESVRNVTFSADYQILGTDNWKKLPAGCOHITSSKCNFSSVELKDVFEKIELRI
RAEEGRNTSTWYTEVBEPPFLKAQIGPDWHLEAEDKAIILSISPPGTEBSLYWALDR
SSFRYSVVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPV
YCINTTERHKVPSPENVQINVDNAYYLKWDYPYESTFQAQNLAFLKKIPGKHSNK
WCQIPMCENVTTHVVFPDISKMGIYYVRVBASNGKOTSFWSEEKEENTEVKPIFP
PVISMKSITDDSLHVSVSASEESENMSVNQLYPLVYEVIFWENTSNAERKVLEKRTDF
TFPNLKPLTVYCVKARALIENDRWNKGSYSOTYCEKTYRGAUSKTWLLAGICTALFS
ILVVIYVVRVFLRCVKYVFFPSKRPSSVDOYFFSDOPLRNLLLSTSEEDTERGFIIEN
ASIITEIEETNEVAEVHEEYNSQASQDSGNYSNEDENSGSKISEEFLQODSV"
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143. .1750
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/product="type 1 interferon receptor"
/protein_id="CaA65183.1"
/db_xref="GI:1213627"
/db_xref="SWISS-PROT:Q28589"
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/db_xref="taxon:9940"
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71. .1753
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Pred. No. 7.3e-177;
D; Mismatches 261;
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                                                                                                                                                      TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTAC
                                                                                                                                                                                                                                 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT
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MUSIFNAR
Mus musculus
cds.
         3894 bp
interferon
          alpha/beta
          receptor (IFNAR) mRNA, complete
                   ROD
                   27-APR-1993
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262 GTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAG
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                                                                                       TGACTTTTTCATTCGATTATCAAAAAACTGGGATGGATAAATTGGATAAAATTGTCTGGGT
                                                                                                                                                                                ACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATG
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                                                                                                                                                                                                                                                  GGGTGCTACCCTCAGCTGCAGGTGGAGAAAATCTGAAACCTCCTGAGAATATAGACGTCT
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Uze,G., Lutfalla,G., Bandu,M.-T.T., Proudhon,D. and Mov
Uze,G., Lutfalla,G., Bandu,M.-T.T., Proudhon,D. and Mov
Behavior of a cloned murine interferon alpha/Deta recei
expressed in homospecific or heterospecific background
expressed in Acad. Sci. U.S.A. 89, 4774-4778 (1992)
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M89641.1 GI:194111
B2 repeat; interferon;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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SVWKYLCHVCFPPLKPPRSIDEFFSEPPSKNLVLLTAEEHTERCFIIENTDTVAVEVK
HAPEEDLRKYSSQTSQDSGNYSNEEEESVGTESGQAVLSKAPCGGPCSVPSPPGTLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLAVVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNY
TLKWSSHGESMGSVYFSAEYERKDEAKWLKVPECQHTTTTKCEFSLLDTNVYIKTQFR
VRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVHISPPGQDGNMWALEK
PSFSYTIRIWGKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSTV
QCISTTVANKHPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPGYSKSSGSHSD
KWKPIPTCANVQTTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPP
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95. .17
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95. .1
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173. 1864
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95. .1867
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/protein_id="AAA37890.1"
/db_xref="GI:194112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPVITVTAMSDTLLVYVNCQDSTCDGLNYEIIFWENTSNTKISMEKDGPEFTLKNLQP
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/db_xref="taxon:10090"
/cell_line="L1210"
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Pred. No. 3.5e
0; Mismatches
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Best Local Similarity
Matches 1343; Conserv
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05-FEB-1990; DO1298.

05-FEB-1990; FR-001298.

(EUBI-) LAB EURO BIOTECHNO.

Eld P. Gresser I. Lutfalla G

TOVEY MG, UZe G;

WPI; 91-319778/44.

P-PSDB; R14487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                014239 standard; DNA; 1343 BP.
014239;
16-JAN-1992 (first entry)
Encodes soluble interferon-alpha/beta receptor.
IFN; autoimmune disease; graft rejection; histocompatibility; ss.
Homo sapiens.
Location/Qualifiers
Key
27, 1337
                                                                                                                                                                                                                                                                                                                                                                                               New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus; Behoet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 10; Page 45; 52pp; French.

The protein encoded by this sequence corresponds to the soluble, extracellular portion of the interferon-alpha and/or beta receptor. The transmembrane and cytoplasmic domains of the native receptor have been deleted to obtain a soluble, circulating form of the protein and the protein and cytoplasmic domains of the native receptor.
                                                                                                                                                                                                                                                                                                                                                        receptor. Potentially immunogenic epitopes have thus been eliminated See also Q14240.
Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;
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In diseases and transplant rejection

Claim 10; Fig 1; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate

Coligonuclectides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q3053), was incubated with oligos (200534 and Q30535. R28496 represents the complete receptor. R28495 captered and cytoplasmic domains. Both forms bind lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.

Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;
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Best Local Similarity
Matches 1343; Conserv
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Sequence encoding a soluble form of the interferon (IFN) receptor
with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon; ss.
Synthetic.
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17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P, Gresser I, Lutfalla G, Meyer
Tovey M, Uze G;
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P-PSDB; R28495.
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Q49625 standard; DNA; 1343 BP.
Q49625;
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Q20-ApR-1994 (first entry)
Q1-ApR-1994 (first entry)
Human interferon receptor extracellular domain coding sequence.
IFN-R; extracellular domain; monoclonal antibody; viral infection;
cell proliferation; allograft rejection; systemic lupus erythematosus;
psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
immunodeficiency; measles virus; interferon-alpha-beta; ss.
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PD 06-OCT-1993.

PF 31-MAR-1992; 400902.

PR 31-MAR-1992; EP-400902.

PR (EUBI-) LAB EURO BIOTECHNOLOGIE SA.

PR (EUBI-) LAB EURO BIOTECHNOLOGIE SA.

PR (EUBI-) LAB EURO BIOTECHNOLOGIE SA.

PR PSDB; R42635 (part).

DR WPI, 93-312951/40.

DR WPI, 93-312951/40.

DR P-PSDB; R42635 (part).

PT Monoclonal antibody to human interferon type-I receptor - having pri neutralising activity against human type I interferon, used for PT neutralising activity against soluble forms of the human CC Unicologie and interferon alpha-beta receptor based on the full-length human IFN-R CC sequence are claimed. (See Q49624 for sequence coding for full-length IFN-R). The antibodies are useful for treatment and CC Inferferon and/or viral
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Best Local Similarity 100.0%;
Matches 1343; Conservative
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WO9507716-A.
23-MAR-1955.
16-SEP-1994; E03114,
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BLOTECHNOLOGIE SA.
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
P-PSDB; R71723
Compsn. of monoclonal antibodies ac useful as immuno:modulator, eg. for Disclosure; F19.2A-2B; 105pp; Engli
                                                                                                                                                                                                                                   Q86457 standard; DNA; 1343 BP. Q86457; Q86457; 16-OCT-1995 (first entry) IFN-R extracellular domain. IFN-R; interferon receptor; interferon-alpha; monoclonal antibody; immunomodulator; AIDS; ss
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Best Local Similarity 99.8%;
Matches 1340; Conservative
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TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                             TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
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                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
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Best Local Similarity
Matches 1334; Conser
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09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
E1d P, Gresser I, Lutfalla G
TOVEY MG, UZE G;
WPJ; 91-319778/44.
P-PSDB; R14488.
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                                                                                                                New water soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The protein encoded by this sequence corresponds to the complete interferon-alpha and/or beta receptor. The invention covers derivatives of the receptor obtained by deleting the transmembrar and cytoplasmic domains of the native receptor or by substitution see also 014239.

Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T;
                                                                                                                                                                                                                                                                                                                                                             Q14240;
16-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                  99.3%; S llarity 100.0%; Conservative 0;
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lisease; graft rejection; histocompatibility;
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In diseases and transplant rejection

Claim 10; Fig 2; S8pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids. Sequence 1755 BP; 593 A; 325 C; 333 G; 504 T;
                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09218626-A.
29-OCT-1992; F00318.
17-APR-1991; W0-F00318.
17-APR-1991; W0-F00318.
(EUBI') LAB EURO BIOTECHNOLOGIE.
E1d P. Gresser I. Lutfalla G. Meyer F.
TOVEY M. UZE G;
WPI; 92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        030533 standard; DNA; 1755 BP.
030533;
31-MAR-1993 (first entry)
Sequence encoding a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon; ss.
Synthetic.
Location/Qualifiers
Key
Location/Qualifiers
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                    TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
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06-CCT-1993:
31-MAR-1992: 400902.
31-MAR-1992: EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
BENO1L P, Maguire D, Meyer F, 1
WPI: 93-312951/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q49624 standard;
Q49624;
20-APR-1994 (fir
                                                                                                                                                                                                                                                                    Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis
Disclosure; Fig 3; 21pp; English.
Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. (See Q49625 for sequence coding for soluble IFN-R, i.e. just the extracellular domain). The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral infection.
Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interferon receptor coding sequence.

IFN-R; extracellular domain; monoclonal antibody; viral infection;
cell proliferation; allograft rejection; systemic lupus erythematosus;
psorlasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
immunodeficiency; measles virus; interferon-alpha-beta; ss.

Homo sapiens.
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CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                       TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAAACACTT
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ilarity 100.0%;
Conservative
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/*tag= a
/product= hIFN-R
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forms of the receptor, 1
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                                                                                                                                                                                                                              score 1334; D
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23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE SJ
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
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Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, &g. for treating AIDS Disclosure; Fig. 38-2B; 105pp; English.

DNA encoding the extracellular domain of the human IFN class I receptor is given in Q86457; the full IFN receptor gene is given in Q86458. Immunomodulator monoclonal antibodies were raised against the recombinant soluble form of the extracellular domain (R71723) expressed in E. coli or COS cell hosts.

Sequence 1755 BP; 592 A; 324 C; 334 G; 505 T;
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Human alpha-interferon receptor protein encoding sequence.

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A (CNRS) CNRS CENT NAT RECH SCI.
A (CNRS) CNRS CENT NAT RECH SCI.
                                                                                                Query Match 99.1
Best Local Similarity 99.9
Matches 1332; Conservative
                                                                                                                                      New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis bisclosure; fig 4; 30pp; French.

This sequence encodes a recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, e.g. where overexpression of alpha-IFN is harmful. The Abs are also useful for e.g. drug targetting. Variants of the protein having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 2784 BP; 896 A; 553 C; 578 G; 757 T;
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:1= glycosylation
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              CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                      CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                       ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
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                                                TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA
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    B
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                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 6; 46pp; English.

A cDNA sequence (T73519) corresponds to nucleotides 1260-1620 of a cDNA clone for human interferon alpha receptor (IFNAR, see also W21804), covering the region that codes for the transmembrane region of IFNAR. Differential splicing of INFAR gene transcripts (see also T73520 and T73521) produces novel soluble, non-membrane bound forms of IFNAR (see also W21805 and W21805) that can be used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                        1269 CTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATACC 1328
                                                                                                           1209 AATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAG 1268
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Transmembranal interferon alpha-receptor cDNA fragment.
Interferon alpha-receptor; IFNAR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1261 ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                      AATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAG 60
    CTGAATAAAAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATACC
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                                                                                                                                                                                                                                                                                360 BP;
                                                                                                                                                                       9.48;
ilarity 100.08;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "primer 171. .82
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/note= "primer:
341. .360
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262. .282
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/note= "exon
10. .30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "exon IX-exon X junction"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "primer 1601. .1619
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                                                                                                                                                                                                                                                                             117 A;
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                                                                                                                                                                                           Score 126; DB 1;
Pred. No. 1.9e-24;
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                                                                                                                                                                                                                                                                             64 C;
                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                             62 G;
                                                                                                                                                                         0;
                                                                                                                                                                                                                 Length 360
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                                                                                                                                                                                                                                                                             117 T;
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RESULT ID 127 PM AC 001 PM
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PA (YEDA) YEDA RES & DEV CO LTD.

PA (YEDA) ABRAMOVICH C.

PA (ABRA)) ABRAMOVICH C.

PI Abramovich C., Ratovitski E, Revel M;

PI Abramovich C., Ratovitski E, Revel M;

PI Holdining, modulating or modifying the activities of interferon(s)

PI New mammalian soluble interferon alpha-receptor forms - used for

PI New mammalian soluble interferon alpha-receptor forms - used for

PI Inhibiting, modulating or modifying the activities of interferon(s)

PS Example 3; Fig 6; 46pp; English.

CC A CDNA sequence (773521) corresponds to a portion of splice-deleted

CC A CDNA sequence (773521) corresponds to a portion of splice-deleted

CC A CDNA sequence (773521) corresponds to a portion of splice-deleted

CC IFN alpha-receptor (IFNAR) form 2 gene transcript, covering a

CC region which, in comparison with transmembranal IFNAR CDNA (see

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC exon IX and of nucleotides 1360-1518, i.e. the end of exon IX and

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC exon IX and of nucleotides 1360-1518, i.e. the end of exon IX and

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC also T73519), has 2 in-phase deletions of nucleotides 1318-1341 in

CC activities of interferons alpha and beta, or for diagnostic

CC activities of interferons alpha and beta, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100
Matches 49; Conservative
                        cds
                                                                                                           cds
                                                                                                                                                                                             cds
                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                            02-JUL-1991 (first entry)
Genes encoding T. hyo 39 k
Swine dysentery; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treponema hyodysenteriae serotype B204.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Q11377 standard; DNA; 6119
Q11377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nomo sapiens.
AU9475977-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T73521 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interferon alpha-receptor splice-deleted form 2 cDNA interferon alpha-receptor; IFNAR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1995.
20-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 BP;
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                      /label= gene 3
/note= "39 kD a
4707. .5859
                                                                                                                                                                                      /note= "39 kn
2067.
                                                                                                                               'label= gene :
'note= "39 kD
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                                                                                                           .4550
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3. 0.0004;
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T W09104036-A.

D 04-APR-1991.

D 04-APR-1990; U05129.

PF 11-SEP-1990; U5-406535.

PR 13-SEP-1989; U5-406535.

PA (MLTE:) ML Technology Ventures.

PI Gabe J, Dragon E, McCaman M;

PR PSDB: R11484, R11485, R11486, R11487.

PT Treponema hyodysenteriae antigens - having molecular wt. of 3 PT and their DNA codes, and use for preparing vaccine.

PS claim 18; Page 49; 84pp; English.

CC The DNA includes family 1 contg. genes 1-4 encoding 39 kD an CC of T. hyo. The sequence was obtd. from clones isolated from CC of genomic library in lambda gtll. The antigens can be exp cand used to prepare vaccines to protect against swine dysent CC see also Q11378-Q11409.

CC See also Q11378-Q11409.

2111 A; 683 C; 990 G; 2323
TA 3223
TA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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Best Local S
Matches 100
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16-DEC-1991; US-808316.

30-JAN-1992; US-828430.

01-FEB-1993; US-014941.

30-SEP-1994; US-315468.

(MYCO) MYCOGEN CORP.
               New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult pests and their larvae Example 3; Column 37-42; 24pp; English.

T43221-T43223 represent the coding sequences for toxins that are active against scarab pests. This sequence was isolated from the Bacillus thuringiensis strain toluvorthi. Insects in the family Scarabaddae constitute a serious pest control problem, especially when destructive larval stage insects infest high value turf found in golf courses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1997 (first entry)
Antiscarab pest toxin 43F coding sequence.
Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae;
larval stage insect; grain; tuberous crop; white grub; c
cyclocephala; popillia; 43F gene; ds.
Bacillus thuringiensis strain tolworthi.
                                                                                                                                                                                                                                                                                                                       Foncerrada L, Michaels WPI; 96-424659/42.
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10-SEP-1996
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nilarity 50.3%;
Conservative
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/note= "39 kD antigen
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Best Local S
Matches 147
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15-FEB-1989; 400428.
15-FEB-1989; EP-400428.
(PLAN-) PLANT GENETIC SI
                                                                                                                                                                                                                                                                                                                                                                                                                          Q05679 stand
Q05679;
Q3-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chafer grubs, and can be found in decaying organic matter, or in the so where they consume plant roots. In Europe and the U.S. populations of these larvae and adults have developed resistance to chemical insecticides such as the organochlorines and DDT. The toxins encoded by these sequences, and intact cells that are capable of expressing the proteins, can be used to control many pests of the family scarabaeidee, such as species of Cyclocephala, and Popillia. The toxins are active against larvae (present in soil) and against adults.

Sequence 1953 BP; 679 A; 323 C; 344 G; 607 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089
             against Coleoptera against Coleoptera against Coleoptera (laim 3; Fig 1; 30pp; English. The BtPGS1208 strain was isolated from grain dust and was deposited at the DSM (19/1/1989) under Acc. No. 5131. The protoxin crystals produced on expression of the gene can be digested with trypsin to produce the mature protein. Plants conty the gene are resistant to Coleoptera pests while the crystals are useful as insecticides.
                                                                                                                                                                                                                                                                                                                                                          btPGS1208 gene.
Toxin; crystal; insecticide; ;
Bacillus thuringiensis strain
Key
Location/Qual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1389
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                                                                                                                                                         Peferoen M, Lambert WPI, 90-255362/34.
                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1209
                                                                                                                          New Bacillus thuringiensis strains -
                                                                                                                                          P-PSDB; R06460
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147; Conserv
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513. .2294
/*tag= b
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Pred. No. 0.25
0; Mismatches
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                                                                                                                          producing
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                                                                                                                     Query Match
Best Local Similarity 44.9
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430 TTATGTAGAAACTAGACCTAGTATAGGATCTAATGATACAATCACTTCCCCCATTTTATGG 1489
                                                                                                                                                                                                                                                                                                                             Bradfish GA, Uyeda KA;
WPI; 93-100566/12.
P-PSDB; R33769.
Controlling lepidopteran pests - using compsn. of Bacillus thuringiensis strains or plants or microorganisms transformed with their toxin genes
Claim 13; Page 25-27; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           together with the btPGS1245 gene (Q05680). Sequence 2425 BP; 872 A; 366 \text{ C};
                                                                                                                                                                                                                                         Claim 13; Page 25-27; 38pp; English.

The sequences given in 028653-55 encode lepidopteran-active toxins. These sequences were used within a Tior Ri plasmid, to transform plant cells. Whole plants can then be regenerated from the transformed cells. The toxin may also be produced by cloning bacillus thuringiensis (Bt). It may then be applied directly to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1992; U07697.
12-SEP-1991; US-758020.
09-SEP-1992; US-941650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1993 (first entry)
Bt isolate 43F coding sequence.
Lepidopteran-active; toxin; Ti;
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1730 AACAGATGAACCACTTGAAAAAGCA 1754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q38654 standard; DNA; 1953
Q38654;
                                                                                                                                                                                                            the plant locus.
Sequence 1953 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MYCO ) MYCOGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTG 493
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374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA 433
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                                                                                                    AGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAC 613
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Search completed: June 1, 2000, 11:12:25 Job time: 19086 sec

AACAGATGAACCACTTGAAAAAGCA 1413

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Title:
Perfect score:
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Maximum DB seq
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US-08-315-468-5
US-08-315-468-5
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US-08-177-755A-8
US-08-178-435-112
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US-08-487-873-112
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## ALIGNMENTS

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Sequence 1, Application US/08307588

Fatent No. 5919433

GENERAL INFORMATION:
APPLICANT: MESTER, Francois
APPLICANT: MAGNIE, Deborah
APPLICANT: MAGNIE, Deborah
APPLICANT: PLAVEC, Tan
APPLICANT: PLAVEC, Tan
APPLICANT: PLAVEC, Tan
APPLICANT: PLAVEC, Tan
APPLICANT: PLAVEC, MICHAELER, ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: MONOCLONAL ANTIBODIES ACTIVITY AGAINST TYPE
CORRESPONDENCE ACDRESS:
ADDRESSEE: POLYS LARIANE
MEDIUM TYPE: Folopy disk
COMPUTER READABLE FORM:
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APPLICATION NUMBER: DE-DOS/MS-DOS
SOSTMARE: MASSISTANCE ANTIBODIES
APPLICATION NUMBER: PC7-DOS/MS-DOS
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FILLING DATE: 30-MS-1993
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Best Local Similarity
Matches 1343; Conserv
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                               TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
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                                                                                                     ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
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Pred. No. 0;
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RESULT 2
US-08-307-588-3
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NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 1728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1755 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Patent No.
                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EI
FILING DATE: 30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MEYER, FIGURE, Deborah
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, MICHAEL G.
APPLICANT: TOVEY, MICHAEL G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                STREET: 3000 CITY: Washington STATE: D.C. 71P: 20007
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIDM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9:
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
Matches 1334; Conserv
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TOPOLOGY: line
MOLECULE TYPE: |
FEATURE:
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100.0%; Pred. No. 0;
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RESULT 3
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: 560-7
FELECOMMUNICATION NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: GRESSER, ION
TITLE OF INVENTION: CDUA
TITLE OF INVENTION: THE A
TITLE OF INVENTION: PREPA
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APPLICANT: UZE, Gilles
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TELEX: 200797 NIXN UR
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 1332; Conserv
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Patent No.
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                                                                      CLASSIFICATION:
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STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
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                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 06-JUN
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    Application US/08466974
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06-JUN-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 1332; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: UZE, Gilles
APPLICANT: UZE, Gilles
APPLICANT: UZE, Gilles
APPLICANT: UZE, Gilles
APPLICANT: GESSER, ION
TITLE OF INVENTION: CONA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1 Patent No.
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APPLICATION NUMBER: US/08/
FILING DATE: 06-7UN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 15-7UN-1992
APPLICATION NUMBER: FR 89/
FILING DATE: 20-0CT-1989
                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4000
TELEYAX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: DUCLEIC acid
STRANDENNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 1332; Conserv
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                               TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
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APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-193
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                      ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ARRAWOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: REPARATION AND USE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND
STREET: 419 Seventh S
CITY: Washington
STATE: D.C.
COUNTRY: USA
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GAAATACCTCTAAA 1386
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th Street, N.W.,
                                                                                                      Version
                                                                                                                                                                                                                       Suite
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US-08-328-256-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Applic Patent No. 5643749
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SEQUENCE CHARACTERISTICS:
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LENGTH: 360 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                           APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-CCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                   NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, INTELE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 12
                                                                                                                                          FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Sever CITY: Washington STATE: D.C.
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                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTAAA 126
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                                   248633
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                                                                                                                                                                                                                                                                                                                                                                                                                                             E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                  202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABRAMOVICH, Carolina RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVEL, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                  TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1953 base pairs
MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1218 CCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCACGCATGGATGAAA 1266
                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MATELECOMMUNICATION INFORMATION: 904-375-8100
                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Process for Controlling Scarab Pests
ITLE OF INVENTION: with Bacillus thuringiensis Isolates
                                                   TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/8
FILING DATE: 30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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49; Conservative 0;
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                                                                 double
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.00.0%; Pred. No.
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No. 5.5e-05;
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ORIGINAL SOURCE:

ORGANISM:

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DNA (genomic)

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                                                                                                               Sequence 47,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
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                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1389 AACAGATGAACCACTTGAAAAAGCA 1413
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                         APPLICATION NUMBER: 08/8 FILING DATE: 20-FEB-1997 ATTORNEY/AGENT INFORMATION:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 TACTTATTGTCTAAAAGTTAAAGCA 638
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                                                                                                                                                                                                                                                                        STREET: 1201 E. CITY: Seattle STATE: WA
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                                                                                                                                                                                                                                           COUNTRY: U:
ZIP: 98102
                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
REGISTRATION NUMBER: 32,743
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5945511
                                                                                                                                                                                                                                                                                                          E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                           USA
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Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                           Jelmberg, Anna C.
Adams, Robyn L.
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                                                                                                                                                                                                                                                                                                                                                                                                          Whitmore,
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: NAME/KEY: Coding Sequence
: LOCATION: 1...1659
: OTHER INFORMATION:
US-08-943-087-47
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Best Local Similarity 49.8%;
Matches 128; Conservative
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                                                                                           COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Slaney, Annette C.
ITLE OF INVENTION: BACILLUS THURINGIENSIS CTYTIIC(b) TOXIN
ITLE OF INVENTION: GENE AND PROTEIN TOXIC TO COLEOPTERAN INSECTS
                                      APPLICATION NUMBER: FILING DATE: 199201 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                     CITY: Philadelphia
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  US 07/649,562
                                                                                PCT/US92/00040
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LOCATION:
PCT-US92-00040-1
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Best Local Similarity 44.9%;
Matches 146; Conservative
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             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                           APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1532 AACAGATGAACCACTTGAAAAAGCA 1556
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                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 TACTTATTGTCTAAAAGTTAAAGCA 638
                                                                                                                                                                      STREET: 2421 N.H. CITY: Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                                                               32606
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US/07/991,867B
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Pred. No. 0.17;
0; Mismatches 179; Indels
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RESULT 12
US-08-107-755A-8/c
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Sequence 8, Application US/08107755A Patent No. 5721352
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/
APPLICATION NUMBER: WO 92/
TIME DATE: 12-FEB-1992
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MOLECULE TYPE:
ORIGINAL SOURCE:
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LENGTH: 1511 base pairs
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PRIOR APPLICATION DATA:
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                                                                                                  755 ATGTTTTCTGGCAAAACAACAGAATTGAT
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Local Similarity 46.1%;
nes 124; Conservative
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                                                                                                                                                                  TTTTTGAAAAATATATCAAATAATAAAAAAAATGTCGATAGAATTAATAATTGGTCCT
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19-FEB-1991
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Pred. No. 0.38;
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T: Moyer, Richard W. T: Hall, Richard L. T: Gruddl, Michael E. INVENTION: No. 5721352el Entomopoxvirus

Expression System

RRESPONDENCE ADDRESS:

ADDRESSEE:

E: David R. Saliwanchik 2421 N.W. 41st Street, Suite A-1

Gainesville

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US-08-107-755A-8
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Best Local Similarity
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                                                                                                                                                                           1022 ACTICCICCAGICITIAACATIAGATCCCTIAGIGATICATICCATATCTATATCGGIGC 1081
1202 AGTTCCTAATTTGAAACCACTGACTGTAT 1230
                                                       1142 TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTAC 1201
                                                                                                                 1082 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
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LENGTH: 1511 base pair
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ORIGINAL SOURCE:
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                           815 TTTTTGAAAAATATATCAAATAATAAAAAAAAAATGTCGATAGAATTAATAATTGGTCCT 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
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                                                                                     ICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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852..1511
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19-FEB-1991
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19-AUG-1993
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30-JAN-1992
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Pred. No. 0.38;
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US-08-544-332-8
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                                                                                                                                                                                                                                                                                                      TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                   FEATURE
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                    FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bencen, Gerar
REGISTRATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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FILING DATE: 07-DEC-1992
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                                   NAME/KEY:
                                                                                    NAME/KEY:
                                                                                                                  LOCATION:
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: 2421 N.W. 41st Street, Suite A-1
Gainesville
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19-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                        Gerard H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l, Michael
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Richard L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             us 07/991,867
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Query Match

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Score 37;

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                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, ver CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/487,890A FILING DATE: 07-JUN-1993 CLASSIFICATION 245
PRIOR APPLICATION DATA: 08/175,116
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/148,968
APPLICATION NUMBER: US 08/148,968
                                                                TELEFAX: (416) 595-1163
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1202 AGTTCCTAATTTGAAACCACTGACTGTAT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1082 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
                                                                                                  TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            962 AAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                     FILING DATE: 08-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Toronto
   STRANDEDNESS:
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o. 5708149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6th Floor, 330 Unviersity Avenue
              1951 base pairs
ucleic acid
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Harkness, Robin
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Klein, Michel
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Yang, Yan-Ping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schryvers, Anthony
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                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                              US/08/487,890A
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0; Mismatches
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; LOCATION: 1..1890
US-08-487-890A-112
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
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                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                       APPLICATION NUMBER: UFILING DATE: 07-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1586 GAATTAATGCAGACTTTAAAAATAATGATAATGCCTTCAAAGGTACAGCAACCGCAGAAA 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1526 TTACCGATAAAAAGCTAACAGGCGAATTAAAACGAGCCGATAATCAAAATACCGTATTTA 1585
                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 AAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTA 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649 CGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATG 708
                                                              APPLICATION NUMBER: US 08/148,968 FILING DATE: 08-NOV-1993
                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 08-NOV-1994
                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sim & McBurney
Suite 701, 330'University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08478435
                                                                                                                                                                                                                                                                                                                                                                                                                Canada
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Klein, Michel
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                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray-Owen, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schryvers, Anthony
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                              Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yan-Ping
   NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pele
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                                                                                                                                      US 08/175,116
                                                                                                                                                                                                         US 08/337,483
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                 24,973
1038-462 MIS:vg
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                                                                                                                                                                                                                                                                                                             Version #1.25
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Search completed: June 1, 2000, 11:11:03 Job time: 19035 sec
                                                                                                                                                                                                                                                                Query Match 2.7%; Score 36.2; DB 4; Length 1951; Best Local Similarity 49.7%; Pred. No. 0.72; Matches 92; Conservative 0; Mismatches 93; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                           1706 AAGTA 1710
                                                                                                                                                            709 AACTA 713
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 1000000
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  4857316 segs, 2026611650 residues
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Gapop 10.0 , Gapext 1.0
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1343
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Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAGGGATCTGCGGCGGC.....ATACCTCTAAATGAGGTACC 1343
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em_est6:*
em_est7:*
           9b_est1: *
9b_est4: *
9b_est4: *
9b_est6: *
9b_est6: *
9b_est8: *
9b_est8: *
9b_est10: *
9b_est110: *
9b_est111: *
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em_est19:*
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em_est15:*
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Million cell updates/sec
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Result
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gb_gss5:*
gb_gss6:*
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em_est26:
gb_est33:
gb_est34:
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gb_est31:
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em_est20:
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gb_est27:
gb_est28:
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em_est28:
em_gss10:
em_gss11:
gb_gss10:
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                                                                                                                                                                                                                                     gb_gssl:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query

DEFINITION CM-HT0152-041099-021-f06 HT0152 Homo sapiens CDNA, mRNA sequence.  ACCESSION AW366810 VERSION AW366810.1 GI:6871460  KEYWORDS EST. SOURCE human. ORGANISM Edazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Mammalia; Eukaryota; Mammalia; Eukaryota; Mammalia; Eukaryota; Mammalia; Comment of the project Unpublished (1999) On Mar 10, 1998 this sequence version replaced gi:2948481. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	6 3.1 1101 83 CNS017ZQ ALIO8704 Drosophi ALIGNMENTS	34 42.8 3.2 597 92 AQ965869  35 42.8 3.2 597 92 AQ965870  36 42.8 3.2 1201 83 CNS0167M  37 42.6 3.2 1101 83 CNS0162P  38 42.6 3.2 1101 83 CNS0161D  39 42.2 3.1 1101 82 CNS0048E  40 42 3.1 1101 82 CNS0047F  41 41.8 3.1 1101 82 CNS0047F  42 41.6 3.1 1097 82 CNS00079  43 41.6 3.1 1101 82 CNS00079  44 41.6 3.1 1101 82 CNS00079  45 AL083479 AL083479 Drosophi  46 AL0 3.1 1097 82 CNS00079  47 AL083479 AL083479 Drosophi  48 AL06 3.1 1101 82 CNS00079  49 AL06 3.1 1101 82 CNS00079  40 AL083479 AL083479 Drosophi  41 AL08 3.1 1097 82 CNS00079  42 AL083479 Drosophi	45.4 3.4 1101 82 CNSODEVL 44.6 3.3 1101 83 CNSO174K 44.6 3.3 1101 83 CNSO174K 44.2 3.3 1001 82 CNSO140O 44 3.3 928 82 CNSO0DKY 43.8 3.3 928 82 CNSO0DKY 43.8 3.3 987 83 CNSO14PQ 43.6 3.2 1101 83 CNSO17KX 43.6 3.2 1101 83 CNSO17KX 43.2 3.2 1101 82 CNSO0PYG 43.2 3.2 781 82 CNSO0PYG 42.8 3.2 579 92 AQ965871	185 13.8 45.2 81 AW435471 AW435471 UI-R-BAL 74.4 13.0 563 29 AA168022 AA168022 MA168022 MS66C03. 45.8 10.9 528 85 AQ684103 AQ684103 HS_2162 45.8 9.6 310 43 AI178178 AI178178 EST22185 58.6 4.4 1101 82 CNS0039G AL063921 Drosophi 56.6 4.2 475 24 H70424 57.6 4.2 475 24 H70424 57.6 58 58 59 81 20 1 101 82 CNS0039G AL063921 Drosophi 58 6 4.2 475 24 H70424 58 6 4.2 475 24 H70424 58 6 59 83 CNS0039G AL063921 Drosophi 58 6 69 83 CNS0039G AL063921 Drosophi 58 6 69 83 CNS0039G AL063921 Drosophi 58 6 69 83 CNS0039G AL063921 Drosophi 58 69 83 CNS0039G AL064084 Drosophi 59 69 83 CNS0039G AL064084 Drosophi 48 6 3 6 101 82 CNS0039G AL064084 Drosophi 48 6 3 6 101 82 CNS0039G AL064084 Drosophi	Score Match Length DB ID  Desci 495.4 36.9 538 80 AW366810 AW36 491.4 36.6 505 30 AA258405 AA25 446.4 33.2 456 79 AW292343 AW2 414.8 30.9 571 46 AI458581 AI4 395 29.4 403 79 AW292342 AW2 365 29.4 403 79 AW292342 AW2 365 29.4 403 31 AA308713 AA3 341.2 25.4 380 30 AA258750 AA25 277.4 20.7 504 33 AA447894 278.6 205.6 15.3 269 21 T96831 T9685
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                      TCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                           AAACATGACCTTTCAAGTTCAGT-GCTCCACGCCTTTTTAAAAAAGGAATCCTGGAACCCA
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                                                                                                    TTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTT
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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On Sep 12, 1996 this sequence version replaced g1:1393828. Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 418.
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4444 Forest Park Parkway, Box 8501, St. Louis,
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Eutheria; |
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314 286 1810
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/clone="1mAGE:667961"
/clone_lib="Soares_NhMMPu_S1"
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Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188431.
Contact: Robert Strausberg, Ph.D.
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www.bio.llnl.gov/bbrp/mage/image.html
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
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EST.
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Email: Robert_Strausberg@nih.gov
The sequence contained an oligo-dT track that was present in the
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/clone=lib="NCI_CGAP_Sub4"
/clone=lib="NCI_CGAP_Sub4"
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/lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-pac (Pharmacia) with a modified
/note="vector: pt7T3D-pac (Pharmacia) with is a subtracted library derived from the is a subtracted library derived from BI. BI constitutes a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP_PT28,
NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_ET22, NCI_CGAP_PT28,
NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_RXid5,
NCI_CGAP_LG12, NCI_CGAP_BT03, NCI_CGAP_RXid1,
NCI_CGAP_LG12, NCI_CGAP_BT03, NCI_CGAP_LG2,
NCI_CGAP_LG12, NCI_CGAP_BT03, NCI_CGAP_LG3,
NCI_CGAP_LG24, NCI_CGAP_LG3, NCI_CGAP_LG3,
NCI_CGAP_LG25, These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
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/db_xref="taxon:9606"
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                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1164 GCTGAGAGAAAAATTATCGAGAAAAAAA 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 CAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACG
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                                                                                                                                                                                                          AI458581 571 bp mRNA
tj97d01.x1 NCI_CGAP_Lu24 Homo sapiens
similar to gb;J03171 INTERFERON-ALPHA
   Eukaryota;
                                Homo sapiens
                                                                                                  AI458581.1 GI:4311160
EST.
                                                                                                                                                         mRNA sequence.
AI458581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_LIB=NCI_CGAP_Lu5
TAG_TISSUE=lung
TAG_SEQ=CAAC"
a 70 c 88 g
   Metazoa;
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Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
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                                                                                                                                                                                                                 CDNA clone IMAGE: 2149441 3' RECEPTOR PRECURSOR (HUMAN);
                                                                                                                                                                                                                    PRECURSOR (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Best Local
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1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGGCCTGTGATCCAGGAT 1118
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                                                                                                                                                                                                                                                                                                                                                           940 TCCGCGTACAAGCATCTGATGGAAATAACACATC-TTTTTGGTCTGAAGAGATAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                505
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                                                                                         TATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATT 1178
                                                                                                                                                                                                                                        GATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGAT
                                                                                                                                                                                                                                                                 GATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCCTTAGTGAT
                                                                                                                                                                                                                                                                                                                                    CCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTTGGTCTGAAGAGATAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATG-CAAAACTACCCAGTGTGTCTTTCCTC-AAACGTTTTCCAAAAAGGAATTT-CCTCT
                                                                                                                                           TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGAT
                                               TATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 5, 1998 this sequence version Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 571)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-Torgan: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LUS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522349). Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soares and M. Fatima Bonaldo.
3 97 c 106 g 194 t
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2149441"
/clone_lib="NCI_CGAP_Lu24"
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Pred. No. 1.6e-91;
0; Mismatches 19
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AW292342/c
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Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188430
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 403)
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www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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//db_xref="taxon:9606"
//clone="IMAGE:2725552"
//clone="IMAGE:2725552"
//clone="IMAGE:2725552"
//clone="IMAGE:2725552"
//clone="IMAGE:2725552"
//lab_bbst="MCI_CGAP_Sub4"
//lab_bbst="M
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3
                                                                     TAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGG
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TTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAA 9
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TAG_LIB-NCI_CGAP_Lu5
TAG_TISSUB-lung
TAG_TISSUB-Lung
TAG_SED-CAAC"
80 g 142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CloneIDs 1257096-1258631, 1469064-1470983, 1475992-1476743) NCI_CGAP_F22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_Col0 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene
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Pred. No. 1.1e-86;
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                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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l (bases 1 to 383)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Man-Wai, C., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., White, O., Sutton, G., Brandon, R.C., Man-Wai, C., Fine, L.D., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J.F., Fine, L.D., Ellips, C.A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Ll, Y.,
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AA308713.1 GI:1961043
EST.
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EST179523 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to interferon, alpha/beta receptor (GB.X60459), mRNA sequence.
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buse) II Homo
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17-MAR-1997

Mammalia;

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les 378; Conserv
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-TTGACTCATTTACACCATTTCG
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                                                                                                                                         ATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTTCTTCATGGTATGAGG
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Humandex (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
12140200
On Sep 12, 1996 this sequence version replaced g1:1392985.
Other_ESTs: THC171186
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/cell_line="KM12C(HCC)metastasis
/note="Vector: pBluescript SK-; specific S
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/db_xref="taxon:9606"
/clone_lib="HCC cell line (matastasis
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                                                                    397
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Pred. No. 1.6e-79;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 380)
1 (bases 1 to 380)
1 (Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rifkin, L., Rohlfing, T., Loan, C., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq.primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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pregnant uterus"
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/clone_lib="Soares_NhHMPu_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., white, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1290666. Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 464.
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis,
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/clone="IMAGE:786130"
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/db_xref="GDB:5983749"
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/dev_stage="8-9 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1135299.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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AI863225
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                                                                                                                                                                                                                                                                                                                                                                                                                                    R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Cente

Clone distribution: NCI-CGAP clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 444)
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                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                       140
                                                                                                                                                                                                                                                                                                                                                       quality sequence stop:
                 /lab_host="PH10B"
// lab_host="PH10B"
// note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall / Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall / Site_2: NotI; This library represents the normalized version of NCI_CGAP_Brn35. Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.19 kb. Tumor types include: meningioma, oligodendroglioma, astrocyt (grade II), medulloblastoma, astrocytoma (grade IV). Constructed by Life Technologies."

Constructed by Life Technologies."
                                                                                                                                                                                                      /clone="IMAGE:2290934"
/clone_lib="NCI_CGAP_Brn52"
/tlssue_type="tumor, 5 pooled (see description)"
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Query Match 20.3 Best Local Similarity 100 Matches 271; Conservative

20.2%;

Score 271; DB 61; pred. No. 2.7e-56; 0; Mismatches 0;

Length 444; indels

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Gaps

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1 (bases 1 to 269)

1 (bases 1 to 269)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Kucaba, T., Le, M., Lennon, G., Marra, M. Holman, M., Hiltman, M., Kucaba, T., Le, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T96831 269 bp mRNA EST 27-MAR-1995
ye51d09.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA cl
IMAGE:121265 5', similar to gb:J03171 INTERFERON-ALPHA RECEPTOR
                                                                                                                                                                                                                                                                                 High quality sequence stops: 210 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 687 Std Error: 0.00 Seq.primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T96831
T96831.1 GI:735455
                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
                                                                                                                                                                                                                                                  quality sequence stop: 210.
Location/Qualifiers
             /db_xref="taxon:9606"
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                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                             /sex="male"
                                                                                                                                                          /clone_lib="Soares fetal liver spleen INFLS'
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    vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                    451 Eckstein Medical Research
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                               Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                             On Jul 8, 1999 this
                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                             discovery
                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW435471.1
                                                                                                                                                                                                                                                                                                                  University of Iowa
                                                                                                                                                                                                                                                                                                                               Program for Rat Gene Discovery and Mapping
                                                                                                                                                                         Seq primer: M13 Forward
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/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia)
                                                  /clone_lib="UI-R-BJOp"
                                                               /clone="UI-R-BJ0p-afu-h-02-0-UI"
                                                                               /db_xref="taxon:10116"
                                                                                            /strain="Sprague-Dawley
                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
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95.5%;
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Pred. No. 2.9e-40;
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   (Pharmacia) with
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611 GACTACTTATTGTCTAAAAGGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTA 670
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Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internat to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

51 c 49 g 75 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAAAAATACACTCTCCTTCCTCCGGTCATTGCTGTCACCCCCACGGGGGACTCCT
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                                                                                                                                                                                                                                                                                                                                               m865C03.rl Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:616516 5' similar to gb:M89641 Mus musculus interferon alpha/beta receptor (MOUSE);, mRNA sequence aA168022
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 563)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                        Theising, B., Wylie, T., Lennon, G., Waterston, R.
The WashU-HHMI Mouse EST Project
  Unpublished (1996)
On Sep 12, 1996 this
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library is a subtracted library derived from the UI-R-AA1,
UI-R-AB1, UI-R-AD1, UI-R-AB1, UI-R-AF1, and
UI-R-AG1 libraries. These libraries represent tissues from
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Pred. No. 3.3e-35;
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                                                                                      Soares, B., Wilson, R. and
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                                                                                                                                                                                     TGTCACCGCCATGAGTGACACCTTGCTTGTTTATGTC------
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                                                                                                                         CTGTCAGGACAGCACATGTGATGGACTCAATTACGAAATCATCTTTTGGGAGAACACTTC
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                                                              CGATACTAAGATAAGCATGGAGAAGGATGGCCCAGA-GTTCACGCTCAAGAGCTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:616516"
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Pred. No. 1.3e-32;
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AI178178 310 bp mRNA
EST21843 NOrmalized rat placenta, Ber
clone RPLCN21 3' end, mRNA sequence.
AI178178
AI178178 1 GI:3728816
EST.
Rattus sp.
M Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2162 row: L column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
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HS_2162_B1_F08_T7C CIT Approved Human Genomic Sperm Library D
Sapiens genomic clone Plate=2162 Col=15 Row=L, genomic survey
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Class: BAC ends
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="Plate=2162 Col=15 Row-L"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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95.5%;
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Pred. No. 1.4e-25;
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RESULT 15
CNS0039G/c
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Best Local Similarity
Matches 169; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTA 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAACACGTCCTTTTGGTCTGAAGAGAAAACTTATTGATTCTCAAAAATACACTCTCCTT
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                             AL063921
AL063921.1
                                                                                                                                                                                                                                                                                                                                                                                                                             CNS0039G 1101 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research 9712, Medical Center Drive, Rockvil Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
Contact: Lee, NH
                                                                                                                                                                           Genoscope
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M.,
Kerlavage, A.R. and Adams, M.D.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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/db_xref="ATCC (1nhost):2033250"
/db_xref="taxon:10118"
/clone="RPLCN21"
/clone="NPLCN21"
/clone="Organ: placenta; Vector: pT7T3Pac; S1 Site_2: Not!"
82 g 85 t
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                                                                                                    segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 KADDDCAGDKDDGKKKADDDTGTKDDDKDKWDDWDKAKGTWGDATWAWAATDWWW 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCT 166
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                                                                                                                                                                                                                                                                                        802 RDRKRADDKRDAADDRDDAATWTTWTTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDDR 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATT--ACTAGTACCAAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
TWAAWTAAAWAAAAAWAATTTTTTTTT 472
                                                                                                                                                                          CAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAAGTTAAAGCAGC 640
                                                                                                                                                                                                                                 WAKWDWKTRADRWDRWAADTWTDARKADRDWAKARAWRARRDRARADRRWTTKGKTT
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                                                      ACTACTTACGTCATGGAAAATTGGTGTCTAT 671
                                                                                                                RDRATWDRTDAWWADAAWWTTTDTDTDDWDKRDRRRKGARRRRRTTARAAWDWWTWKAWD
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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PIR; S14930; S14930.
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HSSP; P02833; ISAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lowney P., Corral J.C., Detmer K., Lebeau M.M., Deaven L., Lawrence H.J., Largman C.;
Lawrence H.S. Largman C.;
"A human Hox 1 homeobox gene exhibits myeloid-specific expression alternative transcripts in human hematopoietic cells.";
Nucleic Acids Res. 19:3443-3449(1991).
                                                                                                                                                                                                                                                                                                 EMBL; X58430; -; NOT_ANNOTATED_CDS.
EMBL; M30599; AAA35006.1; -.
EMBL; S69027; AAD14030.1; -.
EMBL; S69029; AAD14031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio E., Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.; "The human HOX gene family."; Nucleic Acids Res. 17:10385-10402(1989).
                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                 DOMAIN
                                                                                                                                             Transcription
                                                                                                                                                                     PFAM; PF00046; homeobox;
                                                                                                                                                                                PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                           PRINTS; PRO0024; HOMEOBOX
                                                                                                                                                                                                                        MIM; 142957
                                                                                                                                                                                                                                    TRANSFAC;
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                                                                                                                                                         iomeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.

ALTERNATIVE PRODUCTS: TWO ISOFORMS; HOX-A10-1/PL1 (SHOWN HERE)
HOX-A10-2/PL2; ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                     DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                T01713; -.
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                                                                                                                              regulation; Alternative splicing.
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            MISSING (IN ISOFORM HOX-A10-2).
DSL -> MCQ (IN ISOFORM HOX-A10-2).
L -> S (IN REF. 2).
L -> F (IN REF. 2).
R -> P (IN REF. 2).
                                                                                        POLY-PRO.
POLY-ALA.
                                                                              HOMEOBOX
77C6F675916552F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions ong as its content is in
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Maximum DB seq length: 1000000
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Listing first 45
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          protein search, using sw model
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17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
ELID P. Gresser I, Lutfalla G, Meyer
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Mogensen KE, Uze G, Lutfalla G, Gresser
WPI; 91-148740/20.

N-PSDB; Q11701.

New human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human alpha-interferon receptor protein - useful for testin interferon agonists and in treatment or diagnosis Disclosure; fig 4, 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and dinosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when require eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
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IFN agonists; antiviral
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Best Local Similarity
Matches 401; Conserv
31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft
                                     R28496;
31-MAR-1993
                                                            R28496
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Complete interferon-alpha/beta receptor.
IFN; autoimmune disease; graft rejection
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557 AA;
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FR-001298
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Pred. No. 3.3e-185;
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Best Local Similarity 100
Matches 401; Conservative
                                            Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; real proliferation; allograft rejection; systemic lupus erythemato. psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases and transplant rejection.
Claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos (Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids. Sequence 557.AA;
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17-APR-1991;
17-APR-1991;
                                  Homo sapiens.
                                                                                                                                                                        R42635 standard;
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Eid P, Gresser I, Lutfalla G, Meyer F,
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WPI; 92-382110/
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Location/Qualifiers
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06-OCT-1993.
31-MAR-1992;
31-MAR-1992;
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Disclosure; Fig 3; 21pp; English.
Monoclonal antibodies produce& against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
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                                    WO9507716-A.
23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
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IFN receptor; interferon receptor; in
interferon-beta; monoclonal antibody;
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EP-400902.
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EURO BIOTECHNOLOGIE Tovey MG;
                                    EP-402279
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/note- "
                                                                                                            1. .436
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"soluble, immunogenic
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Plavec
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                         SA
                                                                                                                                                                                                         interferon-alpha;
                                                                                                                    _domain
                                                                                                                                                                                          immunomodulator;
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Matches 400
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NPSDB; Q86458.
Compsn. of monoclonal antibodies against interferon rec
useful as immuno:modulator, eg. for treating AIDS
pisclosure; Fig.3A-2B; 105pp; English.
The amino acid sequence of human interferon class I rec
given in R75356. A recombinant soluble form of the ex
c domain of this receptor (R71723) has been used to rais
c immunomodulatory monoclonal antibodies.
Sequence 557 AA;
                                                                                                                                       AU9475977-A.
11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV C
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                 Key
domain
                                                                                                                                                                                                                                                                                                                                                                                                                            spliced-deleted
Interferon alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W21805;
23-SEP-1997
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 2; Fig 7; 46pp; English.

Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (W21805) is characterised by a new domain (S) which follows an
                                                                                               Abramovich C, Ratovitski WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W21805
                                                                                                                                                                                                                                                                                     domain
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/note= "comprises amino a
transmembranal IFNAR"
428. 434
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O; Mismatches
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7.6e-185;
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Best Local S
Matches 400
                                                                                        24-OCT-1993; IL-107378.

(YEDA ) YEDA RES & DEV CO LTD.

(ABRA/) ABRAMOVICH C.

Abramovich C. Ratovitski E, Re
WPI: 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, telssues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembranal interferon alpha-receptor Interferon alpha-receptor; IFNAR.
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  New mammalian soluble interferon alpha-receptor forms inhibiting, modulating or modifying the activities of Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR)
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20-OCT-1994; 075977
24-OCT-1993; IL-107
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16-SEP-1994; E03114.

17-SEP-1994; E03114.

18-SEP-1994; EURO BIOTECHNOLOGIE SA.

18-SEP-1993; EP-402279.

19-SEP-1993; EP-402279.

10-SEP-1993; EP-402279.

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23-MAR-1995.
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IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulato
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Query Match
Best Local Similarity
Matches 398; Conserv

Conservative

99.6%;

Score 2132; DB 1; Pred. No. 1.5e-184; 3; Mismatches 0;

Length 436;

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Gaps

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           Inhibiting, modulating or modifying the activities of interferon(s)

PS Example 3; Fig 7; 46pp; English.

CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2

CC (W21806) is characterised by a double deletion when compared to

CC characterised by a double deletion when compared to

CC shortened by 6 amino acid residues and is followed by a truncated

CC intracellular domain. There is no transmembrane region. The amino

CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.

CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR

CC splice-deleted forms 1 (see also W21805) and 2 may regulate the

CC antagonists or by regulating IFN activities. They can be expressed

CC in host cells and used to inhibit, modulate or modify the

CC activities of IFNs alpha and beta in cells, tissues and organisms,

CC corinocal adagnostic purposes.
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11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRAY) ABRAMOVICH C.
Abramovich C, Ratovitski E, Revel M;
WPI; 95-200634/27.
New mammalian soluble interferon alpha-receptor forms
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PS Claim 2; Page -; 79pp; English.

CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the Crecombinant DNA (I) of the invention. (I) comprises a sequence (S1) CC encoding the interleukin-10 (IL-10) receptor (ILLOR) and a sequence (S2) encoding the interleukin-10 (IL-10) receptor (ILLOR) and a sequence (S2) CC encoding CRFB4, both operably linked to expression control sequences. CC cells containing (I) may be used to identify agonists/antagonist of CC IL-10. Agonists are potentially useful, e.g. for preventing allograft CC rejection, as vaccine adjuvants, for treatment of photosensitivity. CC infiammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, CC viruses, bacteria and parasites (especially intracellular pathogens) and CC for preventing organ rejection. A vector containing (I) is used to CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses a dysfunctional ILLOR and is able to bind IL-10 but not to transduce a containing that expresses CCFB4 sequences (especially ribozymes), can inhibit CL IL-10 activity in cells. Antibodies specific for CRFB4 are used to CC measure and localise CRBF4, for diagnosis of defective IL-10 activity.
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Best Local
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17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
Kotenko SV, Pestka S;
WPI; 98-110590/10.
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                                                                                                                                                                                                                                                                                                          New recombinant DNA - comprises sequences encoding interleukin-10 and CRFB4 linked to operator, useful, e.g. preventing allograft
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Best Local S
Matches 65
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Best Local Similarity
                                                                                                                                                                                                          from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be may be used to treat pathological conditions associated with endogenous IFN-gamma production.

Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA. Agonists/antagonists may be administered parenterally, orally or rectally especially by intravenous injection or directly into a tumour or allograft.
                                                                                                                                                                                                                                                                                                                                                                  Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig.2A; 86pp; English. The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFN-gamma receptor beta-subunit.
Interferon-gamma receptor beta subunit;
interferon-gamma-antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aguet M, Boehni F
WPI; 95-224321/29.
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(HEMM/) HEMMI S.
Aguet M, Boehni R,
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09-DEC-1993; US-164596
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4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
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1 Similarity 30.1%;
65; Conservative
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19. .242
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                                                                        ; Score 199; DB 1; 1; Pred. No. 3.5e-10; 38; Mismatches 81;
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Pred. No. 4.3e-12;
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                                                                          Indels 32;
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63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS

121

96

156

LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD

LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT

LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62

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97

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Query Match Best Local : Matches

85;

Conservative

75;

Score 180; DB 1; Pred. No. 3.8e-08; 5; Mismatches 166

166;

66;

Gaps

15;

Length 553; Indels

Similarity

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                                                        Provided thuman Zeytor7 DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases  
PS Claim 1; Pages 55-59; 72pp; English.

Claim 1; Pages 55-59; 72pp; English.

Chis represents the Zeytor7 cytokine receptor. Zcytor7 is a ligand-binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CRF2). An expression vector containing the Zcytor polypucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transform host cells for the transcriptional terminator and be used to transcriptions of the Scytor7 gene and to isolate ligands binding to it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor7 can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists can also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams RL, Farrah T Whitmore TE; WPI; 98-480798/41.
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02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
(ZYMO ) ZYMOGENETICS INC.
(ZYMO ) ZYMOGENETICS INC.
NAMES RL, Farrah TM, Jelmberg AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zcytor7 cytokine receptor polypeptide.
Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue; agonist; cell proliferation; cell differentiation; renal disease; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W79159 standard; Protein; W79159;
   Sequence
                                   diseases.
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22-AUG-1994; U09438.
20-AUG-1993; US-110119.
(UYNE-) UNIV NEW JERSEY.
COOK JR, Donnely RJ, Em
Pestka S, Schwartz B, SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suppressing tumours in mammals with accessory factor 1 (AF-1) - for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1 DNA in gene therapy Disclosure; Fig 21A; 114pp; English.

The sequence is that of human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant cells. Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9505847-A.
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Interferon-gamma; AF-1; tumour.
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                                                                                                            SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADASTELQQVILISV
                                                                                                                                                                                                                   GPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR
                                                                                                                                                                                                                                                                       GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                               LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFKYTDSK-----WFTADIMSIGV
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                                           -----QNQNYVLKWDYTYANMTFQVQ 234
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Search completed: June 1, 2000, 00:40:12 Job time: 20018 sec

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Title:
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/cgn2_6/ptodata/1/18a/6_COMB.pep:*
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; LENGTH: 434 amino acids ; TYPE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-328-256-11

TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 434 amino acid

TELECOMMUNICATION INFORMATION: 202-628-5197

APPLICATION NUMBER: US/08/328,256
ETILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618

US/08/328,256

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1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60

Query Match Best Local Sim Matches 401;

h 100.0%; Similarity 100.0%; O1; Conservative 0;

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Score 2141; DB 1; Pred. No. 9.4e-214; ; Mismatches 0;

Length Indels

434; 0 Gaps

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3 2 US-08-943-087-44 Sequence 44 3 2 US-08-943-087-46 Sequence 44 3 2 US-08-943-087-54 Sequence 48 3 2 US-08-943-087-56 Sequence 54 1 2 US-08-943-087-50 Sequence 50 1 2 US-08-943-087-50 Sequence 51 2 US-08-943-087-50 Sequence 52 2 US-08-943-087-50 Sequence 52 4 PCT-US94-1427-8 Sequence 54 4 PCT-US94-1427-8 Sequence 61 5 521789-1 Patent No. 5 5 2 US-08-469-537A-103 Sequence 7, 3 1 US-08-727-034-7 Sequence 7, 3 1 US-08-727-034-3 Sequence 7, 3 1 US-08-727-034-3 Sequence 7, 3 1 US-08-727-034-3 Sequence 7, 3 1 US-08-727-034-3 Sequence 7, 4 Carolina Sequence 3, 4 Carolina Sequence 3, 5 CAROLINAENTS  US/08328256  US/08328256  US/08328256  US/08328256  US/08328256  US/08328256  US/08328256  US/08328256  REPARATION AND USE 12 12 12 13 14 15 16 16 16 16 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18
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7-44 Sequence 44 7-46 Sequence 46 7-48 Sequence 46 7-54 Sequence 57 7-50 Sequence 57 7-60 Sequence 57 7-8 Sequence 57 7-8 Sequence 57 7-10-1 Patent No. 57 7-10-1 Sequence 7 7-10-1 Sequence 7 7-10-1 Sequence 3 7
Sequence 44 Sequence 46 Sequence 46 Sequence 56 Sequence 50 Sequence 50 Sequence 50 Sequence 50 Sequence 50 Sequence 10 Sequence 10 Sequence 7, Sequence 7, Sequence 3, Sequence 3, O
Sequence 44 Sequence 46 Sequence 54 Sequence 50 Sequence 50 Sequence 52 Sequence 52 Sequence 7, Sequence 7, Sequence 7, Sequence 3,
Sequence 44 Sequence 46 Sequence 54 Sequence 50 Sequence 50 Sequence 52 Sequence 52 Sequence 7, Sequence 7, Sequence 7, Sequence 3,
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Appl Appl Appl Appl Appl Appl Appl Appl

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RESULT 2
US-08-307-588-2
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                                                                                                                                APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION UNUBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
                                                 TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BENOIT, PATTICK
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
             SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner 3000 K Street, N.W.,
                                                                                                                          17283/117/GUPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite
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US-08-307-588-2
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Matches
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                                             COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: II 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
NAME: BROWDY, ROGER TENES 5610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REVEL, Michel
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CITY: Washington
STATE: D.C.
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nes 401; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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360 326 300 266 240

TELEFAX:

202-737-3528

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SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-256-10
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Best Local :
                                  COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             APPLICANT: GRESSER, ION
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-19
                                                                                                                                                                                 ADDRESSEE: NIXON & V
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STATE: VIRGINIA
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                                         PatentIn Release #1.0,
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 06-JUN-1995
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Pred. No. 1.4e-213;
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                                         #1.25
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GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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                                                                             TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING I
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                                                             NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
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LUTFALLA, Georges
GRESSER, Ion
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Pred. No. 1.4e-213;
; Mismatches 0;
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RESULT 6
US-08-471-453-2
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Best Local S
Matches 401
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TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 anino acids
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APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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TOPOLOGY: lir
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                                                                                        KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                               EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360
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TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 401; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/1370
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: cDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                           27 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
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                                                                                                                                                                                                                                                                                                                                                                 1 GKNIKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                             KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                             EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                       KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
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                                                                                                                                                                                                          Matches 401;
                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-539 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MEYER, Francois,
APPLICANT: MEYER, Francois,
APPLICANT: MAGUIRE, Deborah
APPLICANT: MAGUIRE, Deborah
APPLICANT: TOVEY, MICHAel G.
APPLICANT: TOVEY, MICHAel G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TYPE: Amino acid
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TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 92400902.0 FILING DATE: 31-MAR-1992 ATTORNEY_AGENT INFORWATION: NAME: SAXE, Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/1
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
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                                                                                  61 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                    27 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20007
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                                                                  CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
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                                                                                                                                                                                                                                                                                                                 TYPE: protein
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                                                                                                                                                                                                            Conservative
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Pred. No. 1.
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                                                                                                     Query Match
Best Local :
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                               1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGCQNITSTK 60
              GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
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STRANDEDNESS:

TOPOLOGY: lin

MOLECULE TYPE:
US-08-328-256-12
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US-08-328-256-12
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/328,256
FILLING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILLING DATE: 24-OCT-193
ATTORNEY_MAGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REVEL, Michel APPLICANT: ABRAMOVICH, Carolina APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                    TELEFAX: 202
TELEFAX: 248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDVPLIYEIIFWENTSNAERKIIE
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                                                                                                                                                                                                                             TELEPHONE: 202 - 3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                        LENGTH:
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Score 2089; DB 1,
Pred. No. 2.9e-208;
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Similarity

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Length 496; Indels

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Conservative

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CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI

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                                                                                    ; TOPOLOGY:
PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
              Query Match
Best Local Similarity
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/164596

FILING DATE: 09-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: LOVE, Richard B.

REGISTRATION NUMBER: 34.659

REFERENCE/DOCKET NUMBER: 866PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530
                                                                                                                                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-DECCLASSIFICATION:
                                                                                                                                                                                          TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIXEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360
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Conservative
                                                                                                    linear
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22.9%; Score 490.5; DB 4;
48.5%; Pred. No. 4e-43;
tive 34; Mismatches 69;
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                                   262
                                                                                      203 LPPPENIEVSVQNQNYVLKWDY-TYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVK 261 :| | | :| :| :| | | | | | | | | | : 261
   61
                                                                    1 MPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANVQ 60
                 TTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFH 321
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RESULT 10
PCT-US94-14277-4
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                                                                                              ; TYPE: ami
; TOPOLOGY:
PCT-US94-14277-4
                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Applicati
GENERAL INFORMATION
                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard D
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SPGTKDSYMWALDGLSFTYSLLIWKNSSGYEERIENIYSRHKIYKLSPETTYCLKYKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 NESSLKLNYYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 07-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENLKPPENIDXYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDERKWLKXPECQHTTTTKC
      88; Conserv
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                        20.5%;
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      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 Kb floppy
      Score 438.5; DB 4;
Pred. No. 9.7e-38;
5; Mismatches 68;
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                                          DB 4;
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      Gaps
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
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NAME: Jackson Esq., David A.
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pestka, Sidney ,
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: COTTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 17-JUL-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
   182 TSWKIGVYSPVHCIKTTVENELP 204
                                                          137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                      67 KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
                                                                                                                         79 -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Ave, STREET: Floor
                                                                                                                                                                                                                         7 POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELEPHONE:
                                                    ENEXETWIMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                          PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYXNCQDSTCD-----GLNYEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQAR 173
                                                                                     KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
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                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                               10.3%; Score 220; DB 2; 30.0%; Pred. No. 9.6e-15; tive 41; Mismatches 89;
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                                                                                                                                                                                                                                                                                                Length 325;
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                                             RESULT 13
PCT-US94-14277-6
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                Sequence 6, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/225-5530
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                                                                                                                                                          167
                                                                                                                                                                                          143
                                                                                                                                                                                                                           109 LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: a
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                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/1
FTLING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                 29 LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                 4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                      SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                         VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 197
                                                                                                                                                                                                                                                              DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 142
                                                                                                                       KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRNKAGEWSEPVCEQTTHDETVP 219
                                                                                                                                                                                                                                                                                                                                                                                                      65;
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California
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Aguet, Michel
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 199; DB 4; Length 332; Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Indels

32;

Gaps

APPLICANT:

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US-08-943-087-2
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PCT-US94-14277-6
                                                                                                                                          Sequence 2, Application US/08943087 Patent No. 5945511 GENERAL INFORMATION:
                                   ATEHLOMERAL INFORMALL GENERAL INFORMALL GENERAL INFORMALL GARPLICANT: Lok, Si APPLICANT: Kho, Choon J. APPLICANT: Jelmberg, Anna C. APPLICANT: Jelmberg, Robyn L. Theodore E. Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 8661
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Receptor Subunit Polypeptides NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
APPLICANT: Whitmore Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                   167 SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                        109 LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGYEERIENIYSRHKIY--KL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 07-DEC CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                         64 DITETKCDLTGGGRLKLEPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                            55 NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LARPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                    KPYRVYCLQTERQLILKNKKIRPHGLLSNVSCHETT 214
                                                                                                                                                                                                                                                                                                                                      VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
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SYSTEM: PC-DOS/M9-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1994
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Pred. No. 4.2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98102
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Matches 85; Conserv
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REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206.442-6627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
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LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
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350 PPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESLSRTIPPDKTVIEY 401
                                               335 VIQDYPLIYEI---
                                                                                                                               278 LLRVQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
                                                                                                                                                                                264 ----FLFSVMGYSIYRYIHVGKEKHPANLI----
                                                                                                                                                                                                                                                                       213 LYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKIIFWYVLP----ISITV-----
                                                                                                                                                                                                                                                                                                                  171 TYCLKVKAALLISWKIGVYSPVHCIKTTVENE-------LPPPENIEVSVQNQNY 218
                                                                                                                                                                                                                                                                                                                                                               157 APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1201 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LPKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 96
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LKSPOKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYOKTGMDNWIKLSGCONITSTKCN 62
                                                                                                                                                                                                                      VLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
                                                                                         V----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLND------PQPSGNLR 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 553 amino acids amino acid
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1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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internal
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20.6%; Pred. No. 3.2e-10;
ative 75; Mismatches 166;
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                                          -- IFWENTSNAERKIIEKKTDV--TVPNLKPLTVY 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 11C
CITY: Seattle
CTATE: WA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
                                 219 YLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
                                                                                                        171 TYCLKYKAALLTSWKIGYYSPYHCIKTTYENE-----LPPPENIEVSYQNQNY 218
264 ----FLFSVMGYSIYRYIHVGKEKHPANLI---
                                                                                                                                                                                 122 PGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                63 FSSLKINVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                               37 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                  4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
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REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
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                                                                    LYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKIIFWYVLP----ISITV----
                                                                                                                                               APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT 212
                                                                                                                                                                                                                      LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 156
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Lok, Si
Kho, Choon J.
Jelmberg, Anna C.
Adams, Robyn L.
T: Adams, Theodore E.
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1201 Eastlake Avenue East
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20.6%; Pre
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Pred. No. 3.2e-10;
'5; Mismatches 166; Indels 86; Gaps
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350 PPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESLSRTIPPDKTVIEY 401
                                                  335 VIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV--TVPNLKPLTVY 376
                                                                                                  302 V----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLND------PQPSGNLR 349
                                                                                                                                                  278 LLRYQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
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Search completed: June Job time: 15447 sec 1, 2000, 04:17:53

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Title:
Perfect score:
Sequence:
                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                   Run on:
                                                                              June 1, 2000, 00:37:00; Search time 64.83 Seconds (without alignments) 362.649 Million cell updates/sec
US-09-240-675-2_COPY_27_427
2141
1 GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters:

168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_63:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

30	2 2 8	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	ω	2	_	ŏ.	Result	
110	110.5	111	111	111.5	113	113	113	115	115.5	117	117.5	117.5	117.5	118	118	118	122.5	123	123	123.5	4	199	217.5	220	225	966	1384.5	2141	Score		
	л (л ) ) ()				٠	٠		•													6.9	•	10.2	10.3	10.5	45.1	64.7	100.0	Match 1	Query	<b>,</b>
1912	7160	6839	6831	1896	1767	1615	4	26926	658	817	1585	4	1383	0	981	489	1451	1526	1.3	1443	337	332	349	325	273	590	560	557	Length [		
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A56178	T27935	S57242 .	T27934	T08851	A49502	849502	A44027	I38344	T16040	A48721	T19121	I51669	36	S49015	S51604	A31555	S42167	T13823	T13822	I50600	138500	A49947	G,	A47003	14	528	S27387	A32694	B		
protein-tyrosine-p	, C	œ	hetical prot	Down syndrome cell	protein-tyrosine-p	m	yofibril]	ac G	etical pro	muscle - c	σ		receptor	sin		rferon gamm	tein .	gene	ge	chicke	gamma	gamma	9	recepto	eceptor	alpha/	feron alpha	interferon alpha/b	scription		

# ALIGNMENTS

• • • • • • • • • • • • • • • • • • • •				
QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180	Best Local Similarity 100.0%; pred. No. 4.2e-154;  Matches 401; Conservative 0; Mismatches 0; Indels 0; Ge  1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK	C:Genetics: A:Gene: GDB:IFNAR; IFNAR; IFRC A:Gene: GDB:IFNAR; IFRC A:Gene: GDB:IFNAR; IFRC A:Cross-references: GDB:120078; OMIM:107450 A:Map position: 21q22.1-21q22.1 A:Map position: 21q22.1-21q22.1 A:Introns: 26/1; 67/2; 126/1; 117/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3 A:Introns: 26/1; 67/2; 126/1; 117/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3 C:Keywords: cytokine receptor; glycoprotein; transmembrane protein C:Keywords: cytokine receptor; glycoprotein; transmembrane protein F:1-21/Domain: transmembrane #status predicted <trni> F:437-455/Domain: transmembrane #status predicted <trni> F:437-455/Domain: transmembrane #status predicted <trni> F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate</trni></trni></trni>	A; Notecale type: mRNA A; Residues: 1-557 <uze> A; Residues: 1-557 <uze> A; Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914 A; Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914 A; Cross-reference A; Description: The Structuree of the human interferon alpha/beta receptor gene. A; Reference number: S17112 A; Accession: S17112 A; Accession: S17112 A; Accession: S17112 A; Cross-references: EMBL:X60459; NID:g32671 A; Cross-references: EMBL:X60459; NID:g32671</uze></uze>	RESULT 1 A32694 A12694 C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Accession: A32694; S17112 R:Uze, G.; Lutfalla, G.; Gresser, I. Cell 60, 225-234, 1990 A;Reference number: A32694; MUID:90124632 A. Reference number: A32694; MUID:90124632

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interferon alpha receptor type 1 precursor - bovine (Species: Bos primigenius taurus (cattle) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: $27387; $33770 C;Accession: $27387; $33770 C;Accession: $27387; $33770 C;Accession: $27387; $33770 C;Accession: $27387; $33770 C;Accession: $27387; MUID: $3076908 A;Accession: $27387; MUID: $3076908 A;Accession: $27387
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A;Title: Cloning and characterization of a bovine alpha
A;Reference number: $33770; MUID:93305725
A;Accession: $33770
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421,'V',423-560 <LIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; A;Experimental source: MDBK cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
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                                                                                                                                         LKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFD
                                                                                                                                                                                                                     LLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAF 239
                                                                                                                                                                                                                                                                                                 S-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA 179
                                                                                                                                                                                                                                                                                                                                                                             FSSLKL-NYYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
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                                                             TEIQAFLLPPVFNIRSLS-DSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI 358
                                                                                                                    FKKIPGNHSDKWKQIPNCENVTSTHCVFPREVSSRGIYYVRVRASNGNGTSFWSEEKEFN
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                                                                                                                                                                                                                                                                                                                                                        FSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEAEDKAIILSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                    NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN 85
  IEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                         TEMKTIIFPPVISVKSVTDDSLHVSVGASEESENMSVNQLYPLIYEVIFWENTSNAERKV
                                                                                                                                                                                                LRLQSRVGCYSPVYCINTTERHKVPSPENIQINADNQIYVLKWDYPYENATFQAQWLRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.78;
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Pred. No. 5.5
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interferon alpha/Deta receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Date: 25-Mar-1993 #sequence_revision 18425; I48426; I48427; I48428; I48429 C;Accession: A45283; I48423; I48424; I48425; I48425; I48427; I48428; I48429 B;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 148, 343-346; 1994
A;Title: Structure of the murine interferon alpha/beta
A;Reference number: I48423; MUID:95047447
A;Accession: I48423
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A;Accession: A45283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-590 <UZ
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                                                                                                                                                                     A; Introns: 177/3; C; Keywords: cytoki
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; A;Accession: I48429
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A; Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; A;Accession: I48427
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A; Status: preliminary; translated
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A; Residues: 243-264 <RE3>
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A; Residues: 127-224 <RE2>
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A; Residues: 118-125
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A;Cross-references: EMBL:U06244;
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
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A;Residues: 426-445 <RE6>
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A;Residues: 265-375 <RE4>
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                                               Query Match
Best Local Similarity
Matches 192; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.
Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated
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GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
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                                                                                                                                                                        cytokine receptor;
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                                                    Conservative
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                                                                    45.18;
                                                                                                                                                                          transmembrane protein
                                                                                                                                                                                                                                                                            NID: g497114;
                                               Score 966; DB 2;
Pred. No. 2.3e-65;
1; Mismatches 130;
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                                                                                                                                                                                                                                                                              PIDN: AAA65008
                                                                                              Length 590
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                                                    Indels
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NCBIP: 102357)
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                                                                                                                                                                                                                                                                                 PID:g510265
                                                                                                                                                                                                                                                                                                                                                                                                       PID:g755813
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                                                    10;
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GENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDEAKWLKVPECQHTTTTK

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C;Date: 21-Dec-
C;Accession: GC
R;Lutfalla, G.
                                                                              RESULT
A47003
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A; Residues: 1-273 <LUT>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1994
A;Reference number: G06935
A;Accession: G01418
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokine receptor family II, member 4 -
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision C
C:Accession: G01418
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cytokine receptor family class II protein CRF2-4 precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C;Accession: A47003
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A;Map position: 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:CRFB4; CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 IEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401 : |: ||:||||:|| ||:| ||:|| ||:||
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                                                                                                                                                                                               TSWKIGVYSPVHCIKTTVENELP 204
                                                                                                                                                                                                                                                                           KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
                                                                                                                                                                                                                                                                                                                                                     KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH-ISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSQKHILPPPPVITVTAMSDTLLVYVNCQDSTCD------GLNYEIIFWENTSNTKISM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSKSSSGSHSDKWKPIPTCANVQTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNFSSLKLNYYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH
                                                                                                                                                            DRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                                      ENEXETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                                                                                                                                                                                                                              PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS- 79
                                                                                                                                                                                                                                                                                                                  -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLDDSLHMRFLAPKI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                     POKVEYDIIDDNFILRWNRSDESVGNVTFSFDYOKTGMDNWIKLSGCONITSTKCNFSSL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 225; DB 2; ilarity 30.0%; Pred. No. 7.2e-10; Conservative 43; Mismatches 87;
                                                                                                                                                          219
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C; Accession: JC6311
R; Glbbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A; Title: CRP2-4:isolation of
A; Reference number: JC6311
A; Accession: JC6311
A; Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lutfalla, G.; Gardiner,
Genomics 16, 366-373, 1993
A;Title: A new member of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16.Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-325 <LUT>
                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: A new member of the cytokine receptor gene family A; Reference number: A47003; MUID:93300510
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                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tecal
                                                                                                                                                                                                                7 POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNWIKLSGCONITSTKCNFS
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                                                        QIENEPET----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPWTTYCI
                                                                                                                       --HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLELRFSAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLNYYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT
                           KVKAALLTSWKIGVYSPVHCIKTTVENELPP
                                                                                         ----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL
                                                                                                                                                                                     PEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH-----CKRTASTQCDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENEYETWIMKNYYNSWIYNVQYWKNGIDEKFQIIPQYDFEVLRNLEPWIIYCVQVRGFLP
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61; Conservative
                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                               10.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA clones encoding the human
                                                                                                                                                                                                                                                 45;
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                                                                                                                                                                                                                                               Score 217.5;
Pred. No. 3.7e
45; Mismatches
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                             205
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hes 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A49947
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionalit
A;Reference number: A49947; MUID:94170381
A;Accession: A49947
                                                                                                                                                                                         A;Accession: I38501
A;Molecule type: mRNA
A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; I
A;Experimental source: clone pJS3
                                                                                                                                                                                                                                                                                                                                                   A;Title: Identification and A;Reference number: A49946; A;Accession: I38500
                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapiens (man)
C; Date: 16-Feb-1996 #sequence_revision
C; Accession: 138500; 138501
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                                                                                                                                     A; Map position: 21
C; Keywords: cytokine receptor
                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; A;Experimental_source: clone pSK1
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A; Residues: 1-337 < RES>
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                                                   Local Similarity
mes 62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LKSPQKVEVDIIDDNFILRWNRSDES------VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
LKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL
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                                                                                                                                                                                                             NID: g463551; PIDN: AAA16956.1;
                                                  Score 148; DB 2; Length 337; Pred. No. 0.00062; Mismatches 104; Indels
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C; Species:
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neogenin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I50600
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R;Vielmetter, J; Kayyem, J.F.; Roman, J.M.; Dreyer, W.J.

J. Cell Biol. 127, 2009-2020, 1994

A;Title: Neogenin, an avian cell surface protein expressed

A;Reference number: A55193; MUID:95105243

A;Accession: 150600
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757
                                                                                                                                286 GNNT---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPKQSGNTPVIQDY
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AIGYGI----GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA 796
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                                                                                                                                                                                                                       AFLKRNPGNHL-----YKWKQIPDCENVKTTQCVFPQNVFQ--KGI-----YLLRVQASD 285
                                                                                                                                                                                                                                                                                                               ALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVLKWDYTYANMTFQVQWLH
                                        PLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 382
                                                                                                                                                                                                                                                                       --YNKHGPGVSTQDVVVRTLSDVPSAAPQNLTLEARNSKSIMLHWQPPPA------
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Pred. No. 0.32;
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10

gene protein s: Drosophila

fruit fly (Drosophila melanogaster) melanogaster

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A;Molecule type: mRNA
A;Residues: 1-1375 <KOL>
A;Cross-references: EMBL:U71001; NID:g1621114; PID:g1621115; PIDN:AAC47314.1
C:Genetics:
A;Gene: frazzled
A;Map position: 2
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frazzled gene protein, log isoform - fr
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T13823
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Matches 101
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ROLOddziej, P.A.: Timpe, L.; Mitchell, ell 87, 197-204, 1996

Filtle: Frazzled encodes a Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFEG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR-----
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                                                                                                                                             DVTVPNLKPLTVYCVKARAHT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                          GYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQIT 687
                                                                                                                    MLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                                                                                                CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFTPFRKAQIG-------PPEVHLE-AEDKAIVIHISPGTKDSVMWALD 133
                                                                                                                                                                                                                                                                                              PTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY-----
                                                                                                                                                                                                                                                                                                                                                      GRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVDA
                                                                                                                                                                           ---REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEET
                                                                                                                                                                                                        SDSFHIYIGAPKQSGNTPVIQDYP-----
                                                                                                                                                                                                                                    -HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP------
                                                                                                                                                                                                                                                                                                                                                                                                             -----NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLGW 793
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ilarity 16.3%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                        ; Score 123; DB 2;
; Pred. No. 0.33;
68; Mismatches 18:
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                                       fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                        -LIYEIIFWENTSNAER----KIIEKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodman, C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184;
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               #text_change
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               20-Sep-1999
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C:Accession: S42167

R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, J. Cell Sci. 106, 319-330, 1993

A:Title: The globular head domain of titin extends A:Reference number: S42166; MUID:94095665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, Cell 87, 197-204, 1996
A:Title: Frazzled encodes a Drosophila member of the DC A:Reference number: Z17780
A:Accession: T13823
A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-1526 <KOL>
                                                                                                                 190K protein - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: frazzled
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
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Best Local S
Matches 101
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nes 101; Conserv
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                                                                                                                                                                                                                                                                           MLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                                                                                                                                                    DVTVPNLKPLTVYCVKARAHT
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16.3%; Pred. No. 0.38;
tive 68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID:g1621116; PID:g1621117;
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A:Accession: S42167
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1451 <VIN>
A:Cross references: EMBL:X69090;
C:Superfamily: skelemin
                                                                                                                                                 A;Gene: GDB:IFNGR1; IFNGR
A;Cross references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                          A; Title: Molecular cloning A; Reference number: A31555; A; Accession: A31555
                                                                                                                                                                                                                                                                                                                                                                                                                      Interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-reb-1990 #sequence_revision 28-Fe
C;Accession: A31555
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A; Residues: 1-489 < AGU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 DYIIISWKQPAVDGGSPILGYFIDNCEVGTDSW------SQCNDTPVKFARFPVT 436
201 NELPPPENIEVSVQNQNYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 DNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>1</u>3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSEGIVPGPPTDLSVTEATRSYVVLSWKPPGQRGHEGIMYFVEKCEAGTENWQRVNTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-YKISNLKENMVYQFQVAAMNMAGLGAPSAVSECFKCE 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVKSPRFALFDLAEGKSYCFRVRC----SNSAGVGEPSEATEVTVVGDKLDIPKAPGKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KL-----RIRAEKENTSSW-----YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDITCLESFRDSMVLGWKQPDKTGGAEITGYYVNYREVIDGVPGKWR----EANVKAVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEII----FWENTSNAERKIIEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TCHGLVTGQS------YIFRVRAVNAAGLSEYSQDSE-AIEVKAAIAPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPENIEVSVQNQNYVLKWD------YTYANMTFQVQWLHAFLKRNP-GNHLYKWK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTV-----ENELP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSRNTDTSV-----VVSWEESKDAKELVGYYIEANVAGSGKWEPC--NNNPVKTHRF---
                                                         . Similarity 50; Conserv
                                                         Conservative
                                                                                                                                                                                                                                                                  GB:J03143; NID:g184650;
                                                                         5.5%;
                                                                                                                                                                                                                                                                                                                                          and expression; MUID:89003065
                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 122.5; DB 2;
Pred. No. 0.39;
66; Mismatches 181;
                                                     Score 118; DB 2
Pred. No. 0.19;
39; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g407098; PIDN:CAA48833.1; PID:g407099
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-Feb-1990 #text_change
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                                                                                                                                                                                                                                                                      PIDN:AAA52731.1; PID:g306915
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                                                                                         DB 2;
                                                           102;
                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
                                                                                           Length 489;
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                                                         Indels
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                                                           Gaps
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                                                           10;
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receptor-like tyrosine kinase Ehk-1 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 07-May-1995 #sequence_revision 21 C;Accession: S51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
S51604
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A;Note: the authors translated the codon GAC for residue 170 as Glu
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeate;Seywords: ATP; transmembrane protein
C;Keywords: ATP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re
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A;Molecule type: mRNA
A;Residues: 1-981 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S49015; A; Accession: S51604
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKNLKSPQKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYQKTGMDNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LSDSFH--IYIGAPKQSGN-TPVIQDYPLIYEIIFWENTSNAERKIIEKKTD----
                                                                                                                                                                                                                                            PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR---
                                                                                                                                                                                                                                                                                                                                                                KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH------CIKTTVENELPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ACIALVSVRVYYKKCPSVVRHLAVFPD-----TITGADSSQLLEVSGSCVNHSVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---VIVPNLKPLIVYCVKARA--HIMDEKLNKS-----SVFSDAV 399
                                                                                                                        IRSLSDSFHIYIG---APKQSGNTPVIQ---
                                                                                                                                                                                                                                                                                                                          GFFKASPHSQTCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
                                                                                                                                                                                                                                                                                                                                                                                                          DPPKMHCSAEGEWLV----PIGKCMC--
                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVKTTQCVFPQNVFQKGIYL-LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS--
                                      WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE-----VKNYGVKNSEW--IDACI
FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART
                                                                              VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY
                                                                                                                                                                                                    QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN 312
                                                                                                                                                                                                                                                                                  ---PENIEVSVQNQNYVLKW-------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conserv
                                                                                                                                                            -----YLPQQIGLKNTSVMMADPLAHTNYTF-----EIEA-----VNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 118; DB 2; Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 165;
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A;Molecule type: mRNA
A;Residues: 1-305,'G,',359-1005 <MA2>
A;Residues: 1-305,'G,',359-1005 <MA2>
A;Cross-references: EMBL:588026
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Superfamily: protein tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
F;675-941/Domain: protein kinase homology <KIN>
F;683-691/Region: protein kinase ATP-binding motif
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C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C;Accession: S49015; S51602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:S68024 A;Note: the authors translated the codon GAC for residue 170 A;Accession: S51602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ncogene 8, 3277-3288, 1993
Fifthe: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase Reference number: S49015; MUID:94087777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 5.5%; Score 118; DB 2; Length 1005; Best Local Similarity 20.1%; Pred. No. 0.51; Matches 92; Conservative 51; Mismatches 165; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-1005 <MAI>
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                                                                                                                    449 VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY 508
                                   348 WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 384
                                                                                                                                                                                                                                                                                                                                                                       360 PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR--- 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 DPPKMHCSAEGEWLV----PIGKCMC-------KAGYEEKNGTCQVCRP 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ----ACIALVSVRVYYKKCPSVVRHLAVFPD-----TITGADSSQLLEVSGSCVNHSVTD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG---- 221
509 FEXDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 546
                                                                                                                                                                              253 QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                 206 ---PENIEVSVQNQNYVLKW-------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 GFFKASPHSQTCSKCPP------HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 KIYKLSPETTYCLKYKAALLTSWKIGVYSPVH------CIKTTVENELPP------ 206
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                                                                                                                                                                                                                                            ------YLPQQIGLKNTSVMMADPLAHTNYTF------EIEA-----VNG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 102
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Search completed: June Job time: 14289 sec

1, 2000, 04:35:09

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OM protein - protein search, using sw model

Run

9 :: June

2000, 00:40:17; Search time 34.71 Seconds (without alignments) 351.842 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-240-675-2\_COPY\_27\_427 2141

1 GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE 401

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

83857 seqs, 30454973 residues

Searched:

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	88	7	ō	ري ري	4	ω	2	1		Result
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homo sapien	P48736	PIIG_HUMAN	-	1101	4.3	93	Ü
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rattus norv	P54290	CIC2_RAT	,	1091	4.4	93.5	ü
homo sapien	P20273	CD22_HUMAN	_	847	4.4	93.5	N
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MEDLINE; 95059042.  Colamonici O., Yan H., Domanski P., Handa R., Smalley D., Mullersman J., Witte M., Krishnan K., Krolewski J.; "Direct binding to and tyrosine phosphorylation of the alpha subunit of the type I interferon receptor by p135tyk2 tyrosine kinase."; Mol. Cell. Biol. 14:8133-8142(1994).  MOI. Cell. Biol. 14:8133-8142(1994).  I FING TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA- SUBUNITS THEMSELVES.  I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN  I TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.  I SUBCELLULAR LOCATION: TYPE IFN-RESISTANT CELLS.  I SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  I SIMILARITY: SELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  EMBL: J03171; AAA52730.1;  EMBL: J03171; AAA52730.1;  EMBL: J03172; SA7112.	. tp 900.	

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INTERFERON-ALPHA/BETA REC.

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NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN NLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN

FSSLKL-NYYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI FSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEAEDKAIILSI

120 85 62

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LIM J.-K., Langer J.A.;
Lim J.-K., Langer J.A.;
Cloning and characterization of a bovine alpha interferon receptor.";
Cloning and characterization of a bovine alpha interferon receptor.";
Biochim. Biophys. Acta 1173:314-319(1993).

I FORCION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
SUBUNITS THEMSELVES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOXINE FAMILY OF RECEPTORS.
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SIGNAL
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EMBL; L06320; AAA02571.1;
PIR; S33770; S33770.
PIR; S27387; S27387.
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Specific antiviral activities of the human alpha interf determined at the level of receptor (IFNAR) structure."; FEBS Lett. 313:255-259(1992).
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Mouchel-Vielh E.,
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

*Molecular cloning of ovine and bovine type I interferon recep
subunits from uteri, and endometrial expression of messenger
ribonucleic acid for ovine receptors during the estrous cycle
pregnancy.*;
Endocrinology 138:4757-4767(1997).

FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING
                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AN
SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED
CONCEPTUS AT DAY 15 OF PRECNANCY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAI
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF
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OKINE FAMILY OF RECEPTORS.
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR
IFNAR1 OR IFNAR OR IFAR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurognat
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Lutfalla G., Gardiner K., Uze G.
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CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
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- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1994 (Rel. 35, Last annotation update)
INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
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                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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     SEQUENCE
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PFAM; PF00041; fn3;
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SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBGELLULAR LOCATION: TYPE INTERFANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTO
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01-0CT-1996
15-JUL-1999
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P52179;
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"The globular head domain of titin extends into the center of sarcomeric M band. cDNA cloning, epitope mapping and immunoel microscopy of two titin-associated proteins.";
"J. Cell Sci. 106:319-330(1993).
"J. CELL Sci. 106:319-330(1993).
"ISSOCIATION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING I
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                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhin;
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MEDLINE; 94095665.
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6 (Rel. 34, Last sequence update)
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR
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                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                           SEQUENCE FROM N.A. MEDLINE; 89003065. Aguet M., Dembic Z
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  receptor.";
Cell 55:273-280(1988).
                                                                                                                                          Eutheria;
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                                "Molecular cloning and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGTKDSVMWALDGLSFT----YSLLIWK-----NSSGVEERIENIYS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPENIEVSVQNQNYVLKWD-----YTYANMTFQVQWLHAFLKRNP-GNHLYKWK
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                                                                                                                                          Primates;
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                                                                                                                                            Catarrhini;
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                                                             Merlin
                                         expression
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 122.5; DB 1; Pred. No. 0.18; 5; Mismatches 181;
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6.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                              Craniata;
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                            Hominidae;
                                           of.
                                           the
                                                                                                                                                                                                                                                                                                                       489
                                                                                                                                                                Vertebrata;
                                                                                                                                                                                                                                                                                                                       ₹
                                           human
                                                                                                                                              Homo
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                                             interferon-gamma
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8 20

27

50;

Conservative

39;

102;

Indels

34;

Gaps

10;

Similarity

SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE---

-VKNYGVKNSEW--IDACI 78

201 NELPPPENIEVSVQNQNYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE 258

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Query Match
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Matches 50
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J. Mol. Biol. 273:882-897(1997).

-:- FUNCTION: RECEPTOR FOR INTERFERON GAMMA TWO DEFORMATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
MEDLINE; 93183911.
Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gar
"Alignment of disulfide bonds of the extracellular domain
"nterferon gamma receptor and investigation of their role
biological activity.";
Biochemistry 32:2423-2430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zauodny P.J., Narula S.K.; "Crystal structure of a complex between interferon-gamma soluble high-affinity receptor."; Nature 376:230-235(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walter M.R., Windsor W.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERFERON-GAMMA DIMER.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY
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                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                   Transmembrane;
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489
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COCF9E574D8F47400 CRC64;
 Score 118; DE Pred. No. 0.09
                                                                                                                                                                                          INTERFERON-GAMMA RECEPTOR EXTRACELLULAR (POTENTIAL) POTENTIAL. CYTOPLASMIC (POTENTIAL).
             No. 0.093;
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                                                                                                                                                                                                                               RECEPTOR
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                           Length 489
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPA5_RAT P54757;
HSSP; P00523; 2PTK.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00109; TYRKINASE_ATP; FA
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                  EMBL; X78689; CAA55357.1;
HSSP; P00523; 2PTK.
                                                                                                                       use by non-profit institutions as long as its cont
modified and this statement is not removed. Usage by
entities requires a license agreement (see http://www.
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                     "Expression and developmental regulation of Ehk-1, a neuronal Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor V., Pfarr S., Mie
Lassmann H., Steck A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
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Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95206467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                       EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
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Rattus.
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                                                                                            253
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                                                                                                                                                                                                                                                                                                                                         165 GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG----
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            VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY
                                                                                                                                                                                                                                                 GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH
                                       IRSLSDSFHIYIG---APKQSGNTPVIQ-------DYP----LIYEIIF
                                                                                                                                      ---PENIEVSVQNQNYVLKW------DYTYANWTFQVQWLHAFLKRNPGNHLYKWK
                                                                                          QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN
                                                                                                                                                                          GFFKASPHSQTCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPTMACTRP
                                                                                                                                                                                                     KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH------CIKTTVENELPP-----
                                                                                                                                                                                                                              DPPKMHCSAEGEWLV----PIGKCMC------KAGYEEKNGTCQVCRP
                                                                                                                    PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR---
                                                                                                                                                                                                                                                                                    ----ACIALVSVRVYYKKCPSVVRHLAVFPD----TITGADSSQLLEVSGSCVNHSVTD
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PF01404; EPH_1bd; 1.
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Glycoprotein; Signal; Alternative splicing
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SPLICED FORMS).
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G -> A (IN REF. 2
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ATP (BY SIMILA
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Length 1005; Indels 150;

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                                          PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKIMASE.

PROSITE; PS00107; PROTEIN_KIMASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KIMASE_TYR; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS50011; PROTEIN_KIMASE_DOM; 1.

PROM; PF00041; fn3; 1.

PFAM; PF000575; FURIN-11ke; 1.
                                                                                                                                                                                                  EMBL; U80631; AAB3896
EMBL; U80630; AAB3896
EMBL; U80629; AAB3896
PIR; A36080; A36080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein B.J., Dudley A.L.;
"The rat insulin receptor: primary structure and conservation tissue-specific alternative messenger RNA splicing.";
Mol. Endocrinol. 4:235-244(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LICAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE PHOSPHATE. ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES
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Tyrosine-protein kinase; Receptor; Transmembrane;
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PFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
OMW; E313C7D39FE6CAC7 CRC
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                                         -RIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAED-
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                   Score 113;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                         EL SUBMITTED (JUN-1996) to the EMBL/GenBank/DDBJ databases.

10 - FUNCTION: IMPLICATED AS A TUNGEN SUPPRESSOR GENE.

11 - FUNCTION: TYPE I MEMBRANE PROTEIN.

12 - I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ARE PRODUCED FROM THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY ALTERNATIVE SPLICING.

12 FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO AT HIGH LEVELS IN THE EMBRYO EXPRESSED AT HIGH LEVELS IN THE EMBRYO EXPRESSED AT HIGH LEVELS IN THE EMBRYO EXPRESSED AT HIGH LEVELS IN THE EMBRYO EXPRESSED IN THE EMBRYO EXPRESSED IN THE EMBRYO EXPRESSED IN THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED IN THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF THE EMBRYO EXPRESSED OF T
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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
EMBL; X85788; CAA59786.1;
HSSP; P56276; lTLK.
MGD; MGI:94869; DCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of the mouse homologue of the deleted in colorectal can gene (mDCC) and its expression in the developing mouse embryo."; Oncogene i1:2243-2254(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooper H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-BRAIN;
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STRAIN-BALB/C; TIS
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J. Biol. Chem. 270:6722-6728(1995).

[2]
[2]
SEQUENCE OF 300 101
                                                      PROSITE; roughly fina; v. PRAM; PF00041; fna; v. PFAM; PF00047; 1g; 3. PFAM; PF00102; Y_phosphatase; 2. PFAM; PF00102; Y_phosphatase; 2. Pram; PF10102; Y_phosphatase; 2. Pram; PF10102; T. POTENTIAL. POTENTIAL.
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Eutheria; 1
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TRANSMEM
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR
                                                                                                                                                                                                                                                                                   EMBL; L38929; AAC41749.1;
EMBL; X54133; CAA38068.1;
PIR; S12052; S12052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOS
PROTEIN TYROSINE + ORTHOPHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PRO
ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS
TISSUES DUE TO ALTERNATIVE SPLICING.
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE
FROM THE TRANSMEMBRANE SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IGLIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
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PRTYPHPHTASE
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TYR_PHOSPHATASE_2; 2.
TYR_PHOSPHATASE_PTP;
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evolution
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Best Local
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061727;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, PRECURSOR (IL-10R).
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MEDLINE; 94068585.

HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Mc Ho A.S.-Y., Interferon To interferon Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).

-!- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIC
                                                                                          INTERLEURIN-10 RECEPTOR PRECURSOR (IL-10R).
IL10RA OR IL10R.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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22.9%;
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PROTEIN-TYROSINE PHOSPHATASE.

BY SIMILARITY.

BY SIMILARITY.

CLEAVAGE (POTENTIAL).

POTENTIAL.

POTENTIAL.

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MISSING (IN KIDNEY ISOFORM).

MISSING (IN KIDNEY ISOFORM).

MISSING (IN KIDNEY ISOFORM).

MISSING (IN KIDNEY ISOFORM).

MISSING (IN FETAL BRAIN ISOFORM).

MISSING (IN FETAL BRAIN ISOFORM).

R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.

9 MW; JAEBCBCD32182E26 CRC64;
                                                                                                                                                                                                                                                                                               384
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
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Pred. No. 2.2;
24; Mismatches
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on receptors
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EPA5_HUMAN STANDARD; PRT; 1037 AA. P54756; P64756; P64
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SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEIKFOTEIQAFLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDEVIL-----TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQVFKDLRVYKISIRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- KLPTVLVFKKPHDFFPANPLCPETPDAIHIVDLEVFPKVSLELRDSVLHGSTDSGFGS
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75; Conservative
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INTERLEUKIN-10 RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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                                                                               annotation update)
ECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

;

Length 1037;

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PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOW; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOW; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01106; EGF_2; UNKNOWN_1.

PFAM; PF00041; fin; 2.

PFAM; PF00069; PKINASE; 1.

PFAM; PF0005; SAM; 1.

PFAM; PF00106; SAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miescher G.C.
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                               CARBOHYD
CARBOHYD
                                                               CARBOHYD
CARBOHYD
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EMBL; L36644;
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                                                                                                                                                                         CHAIN
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                                                     CARBOHYD
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 SEQUENCE
                     VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARI ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM
                                                                                                                                                                                                                                                                                                                                                    600004
                                                                                                                                                                                                                    PF01404;
                                                                                                                                                                                               Transmembrane;
 1037
                     Tyrosine-protein
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; SAM; 1.
; EPH_lbd; 1.
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Glycoprotein; Signal; Alternative splicing
POTENTIAL.
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                               POTENTIAL.
POTENTIAL.
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POTENTIAL.
                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                              EPHRIN TYPE-A RECEPTOR 5. EXTRACELLULAR (POTENTIAL).
                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                       POTENTIAL.
                     SCCECGCGRASSLCAVAHPILIW -> R
                                                                                      POTENTIAL.
                                                                                                  SIMILARITY.
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                                                                                                                                                                                                                                                                 KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH------CIKTTVENELPP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GKNLKSPQKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYQKTGMDNW 47
                                                                                                                                             HIYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFL
                                                                                                                                                                                                        ---PENIEVSVQNQNYVLKW------DYTY----ANMTFQVQWLHAFLKRNPGN
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                                                         ---VNGVSDLSPGARQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIIL
                                                                                                                                                                                                                                       GFFKASPHIQSC------GKCPPHSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
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EYEIKHFEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 544
                       IYEIIFWENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT
                                                                                     LPPVFNIRSLSDSFHIYIG---APKQSGNTPVIQ-------
                                                                                                                   HV---RYLPRQSGLKNTS-------VMMVDLLAHTNYTF------EIEA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108; DB Pred. No. 1.4;
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Perfect score:
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Maximum DB seq length: 1000000
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## ALIGNMENTS

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208 KVQATVPLEDKGGLFSPIHCIKTTRKVNDLLCPTNVRVFALNMKFYLLMDNHYNEHVTYT 267	175 KVKAALLTSWKIGVYSPVHCIKTTVE-NELPPPENIEVSVQNQNYVLKWDYTY-ANMTFQ 232	150 KINISPPEANQVRKMW-LISVFFKYNVVIWDNSSNV-EKVRSILPIDVINDLAPETTYCL 207	(7)	90 HTECDESSAITAYYDTHHIRIRAERREAKSPWSSIFEMIPYEIAQIGPPEIALQSINGAI 149	58 STKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSSTPFRKAQIGPPEVHLEAEDKAI 116	31 NIKSPODIQVYAVNTNETIMMNYTGDGT-NVTFSAQYQCFDDLQTSEPEWKELSGCQNVS 89	DIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWI	Query Match 31.2%; Score 668.5; DB 13; Length 569; Best Local Similarity 38.0%; Pred. No. 8.9e-46; Matches 158; Conservative 77; Mismatches 154; Indels 27; Gaps 12;	SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;		EMBL: AF082664: AAD13669 1:	Genome Res. 0.0-0(1999)	recent rest yearsman analysis of the interferent in threatenanting to	ON D.,	TISSUE-LIVER;	SEQUENCE FROM N.A.	Neognatnae; Galliformes; Phasianidae; Phasianinae; Gallus. [1]	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;	Gallus gallus (Chicken).	IFNAR1.	Last	(TrEMBLrel. 10, Last	-1999 (TrEMBLrel.	Q9YHWO: PRELIMINARY; PRT; 569 AA. O9YHWO:	LT 1

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Matches 60
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EMBL; U53696; AAC53062.1; -

MGD; MGI:109380; II10rb.

PFAM; PF00041; fn3; 1.

SEQUENCE 349 AA; 39774 N
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
CYTOKINE RECEPTOR FAMILY 2,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                            01-NOV-1996
01-NOV-1996
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"CRF2-4: isolation of c
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                  Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                     IFNGR2
                                                                                                            INTERFERON
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(TremBLrel. 01, Last sequence update)
(TremBLrel. 12, Last annotation update)
CEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
                                                                                                          6 (TrEMBLIEL. 01, (6 (TrEMBLIEL. 01, I) 9 (TrEMBLIEL. 12, I) GAMMA RECEPTOR 2
                                                                                                            GAMMA
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(INTERFERON GAMMA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 216.5; DB pred. No. 8e-10; 45; Mismatches 7
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Best Local S
Matches 65
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EMBL; U69599; AACS2938.1; JOINED.
EMBL; U69594; AACS2938.1; JOINED.
EMBL; U69596; AACS2938.1; JOINED.
EMBL; U69596; AACS2938.1; JOINED.
EMBL; U69597; AACS2938.1; JOINED.
EMBL; U69598; AACS2938.1; JOINED.
EMBL; U69598; AACS2938.1; JOINED.
EMBL; U69598; AACS2938.1; JOINED.
REBOUL J., GARDINER K., MONNERON D
"Comparative genomic analysis of tl
receptor gene cluster.";
Genome Res. 0:0-0(199).
EMBL; AF08266; AAD13678.1;
EMBL; AF082666; AAD13671.1;
Receptor.
RECEPTOR.
RECEPTOR.
SEQUENCE 341 AA; 39062 MW; 7433
                                                                                                                                                                                                                                                                                                      Q9YGC8 PRELIMINARY;
Q9YGC8;
01-MAY-1999 (TTEMBLTel. 1
01-MAY-1999 (TTEMBLTel. 1
01-MAY-1999 (TTEMBLTEL. 1
INTERLEUKIN-10 RECEPTOR 2
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMMI S., BOHNI R., STARK G., DI MARCO "A novel member of the interferon recept functionality of the murine interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-129SV/J;
MEDLINE; 97128072.
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MEDLINE; 94170381
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                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                  IL10R2.
                                                                                                                                                                           SEQUENCE FROM N.A.
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; PF00041; fn3;
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Pred. No. 1.9e
88; Mismatches
                                                                                                                                                                                                                                                                                                                              Created)
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interferon/interleukin-10
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L.9e-08;
hes 81;
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Gallus.
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Best Local :
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Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Eukaryota; Metazoa; Chordata; Craniata; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (Tremblrel 12,
01-NOV-1999 (Tremblrel 12,
01-NOV-1999 (Tremblrel 12,
GLYCOPROTEIN 130 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                 GEISSEN M., HELLER S., PENNICA D., ERNSBERGER U., ROHRER H.; "The specification of sympathetic neurotransmitter phenotype depends on gpl30 cytokine receptor signaling."; Development 125:4791-4801(1998).
EMBL; AJ011688; CAB42084.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 99026068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6U9;
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                     387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 CIKTTVENELPPPENIEVSVQNQNYVLKWD---YTYANMTFQVQWLHAFLKRNPGNHLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 8.6%;
Local Similarity 26.9%;
hes 59; Conservative /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVNVKSESGTLHVDFTGPAADREHDKWSLKQYYGSWIYRILYWKKGSN--KKVIHIDTKH
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                                  GKLWVGWTAPNNVLKYVIEWC---LMSNSSDCITEWQTEPG--NI-----QGTYLKG
                                                       ONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKG
                                                                                  YNVTTTSLTLKLPNGTY----EVTVVAHNRVGA-SPPSVLLIPSSNSKAPVKNIRTLPKD
                                                                                                        HKIYKLS----PETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN
                                                                                                                                                                                   SIQGLRPYTEYVFSIRCMKEDGVGFWSDWSE------EQIG-----VTTEDKP----
                                                                                                                                                                                                          SSLKLNVYEEIKLRIRAEKEN----TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH
                                                                                                                                                                                                                                  PRNLSYNSGILPTVLKLSWENQISTVVMELKFNIRYRISSDINWMEVPP-EDTASPRTSF
                                                                                                                                                                                                                                                PQKVEVD--IIDDNFILRW-NRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNF
                                                                                                                                  ----SKGPTIWRTIDVSPSPAFWIVRLMWKALEPFEANGVILQYEVTIRAKPPLSHPPSR
                                                                                                                                                         ISPGTKDSVMWALDGLS----FTYSLLIWK----NSSGV------
                                                                                                                                                                                                                                                                                             Similarity
---IXLLRVQA---SDGNNTSFWSEEIKFDTEIQAFLLP-----PVFNIRSLSDSFH
                                                                                                                                                                                                                                                                                                                                              918 AA;
                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                              26 POTENTIAL.
102495 MW; 9DC128C3
                                                                                                                                                                                                                                                                                             6.2%;
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Pred. No. 3.4e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                 Score 133.5; DB 13;
Pred. No. 0.013;
7; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           918
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                                                                                                                                                                                                                                                                                                                                              CRC32;
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                                                                                                                                                                                                                                                                                  105;
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O9YHV9; O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 10, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative genomic analysis receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1; -.
HSSP; P13726; 1TFH.
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE NEOCENIN (FRACKENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Arc
Neognathae; Galliformes; Phasianidae; Phasianinae; Gal
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EMBL; Y09535; CAA70727.1; -.

HSSP; P02751; 1TTG.

MGD; MGI:1097159; Neo1.

PFAM; PF00041; fn3; 6.

PFAM; PF00044; FNTYPEIII.

SEQUENCE 1493 AA; 163159 MW; 98F266
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P97798;
01-MAY-1997
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                             AIGYGI---
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SEQUENCE FROM N.A.
MEDLINE: 970.5076.
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EMBL; U07644; AA
HSSP; P80362; IW
PFAM; PF00041; f
PFAM; PF00047; I
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Q94537;
01-FEB-1997
01-FEB-1997
01-NOV-1999
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J. Cell Biol. 127:2009-2020(1994).
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VIELMETTER J., ROMAN J.M.,
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STRAIN-WHITE LEGHORN;
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                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                       FRAZZLED.
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                                                                                                                                             MITCHELL
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Pred. No. 0.15
50; Mismatches
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Last sequence up
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Best Local
SEQUENCE FROM N.A.
MEDLINE; 970.15076.
KOLODZIEJ P.A., TIMPE L., M
JAN L.Y., JAN Y.N.;
"frazzled encodes a Drosoph
                                                                                                                                                                                                                                                   Q94538;
Q94538;
Q1-FEB-1997;
Q1-FEB-1997;
Q1-NOV-1999;
                                                                                                                                                                                                              FRAZZLED.
FRAZZLED.
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PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1375 AA; 151692
                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1017
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01; Conservative
                                                                                                                                                                                                                                                   (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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16.3%;
                                        MITCHELL K.J.,
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Pred. No. 0
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      member
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                                           GOODMAN C.S.,
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a; Brachycera; Muscomorpha;
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Best Local S
Matches 101
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FLYBASE; FBgn0011592; fra.
FFAM; FP00044; fn3; 6.
FFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1526 AA; 168787 M
                                                                                                 01-FEB-1997
01-FEB-1997
01-NOV-1999
                                                                                                                                           Q92859
Q92859;
                                                                                                                                                                                                                               1168
                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        1111
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              SEQUENCE FROM N.A.
                                                                                      NEOGENIN
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(TrEMBLrel. 02, Last sequence u)
(TrEMBLrel. 12, Last annotation
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Query Match
Best Local Similarity
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EMBL; U61262; AAB17263.1; -
HSSP; P02751; lTTG.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1461 AA; 159958
                                                         Genomics 41:414-421(1997).
EMBL; U72391; AAC51287.1; -.
HSSP; P02751; ITTG.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; ig; 4.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                      000340; PRELIMINARY;
000340; TIEMBLEL 04,
01-JUL-1997 (TIEMBLEL 04,
01-JUL-1997 (TIEMBLEL 12,
                                                                                                                                                       MEDLINE; 97312699.
VIELMETTER J., CHENG X.N., MISKEVICH VIELMETTER J.R., DREVER W.J.;
"MOLECULAR Characterization of human
                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                SEQUENCE
                                                                                                                                 and
q23
                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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33; Conservative
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                                               1461 AA;
                                               FNTYPEIII.
AA; 160015
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Pred. No. 0.24;
77; Mismatches 188; Indels 5
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HSSP; P56276; 1TLK.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 19; 4.
PRINTS; PR00014; FNTYPEIII.
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Q91562;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 95113183.
PIERCEALL W.E., REALE M.A., CANDIA A.F.,
FEARON E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR SUPPRESSOR
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Rhabditina; Rhabditoidea; Rhab
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VVSDLNAHKP--YAFCVLAVKNNRQGPCSDP---PTVLES--VTPTYMVQNLRVLWKTSN
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Rhabditidae; Peloderinae; Caenorhabditis
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C -!- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL RECEPTOR. BINDS LDL,

C MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA, AND TRANSPOR

C IT INVO CELLS BY ENDOCYTOSIS.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SIMILARITY: CONTAINS IN PAACENTA, LIVER, MIDHEY AND PANCR

C -!- SIMILARITY: CONTAINS SIX FIBRONECTIN TYPE III-LIKE DOMAINS.

C -!- SIMILARITY: CONTAINS SIX FIBRONECTIN TYPE III-LIKE DOMAINS.

R EMBL; VO8110; CAA65091.2; -.

R EMBL; VO8110; CAA65091.2; -.

R EMBL; FF00055; AAC5091.2; -.

R FFAM; PF00056; 1dl_recept_a; 11.

R PFAM; PF00058; 1dl_recept_b; 4.

P FFAM; PF00051; Inl_recept_b; 4.
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01-JUN-1998 (TIEMBLrel. 06, I
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"Molecular characterization of a novel Numan hybrid-type receptor binds the alpha2-macroglobulin receptor-associated protein.";
J. Biol. Chem. 271:31379-31383(1996).
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HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vei
Eukaryota; Primates; Catarrhini; Hominidae;
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MORISAKI N., NIMPF J., SCI
Arterioscler. Thromb. Vasc
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RECEPTOR-RELATED PROTEIN LR11
EXTRACELLULAR.

LDL-RECEPTOR CLASS I

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PT diseases and transplant rejection

CC Laim 2; Fig 1; 58pp; English.

CC DNA encoding the water-soluble polypeptide with a high affinity for CC IFN-alpha and -beta is isolated by PCR, using appropriate

CC digonucleotides as primers and cloned CDNA as template. For example, CC the IFN-alpha and -beta receptor (030534), was incubated with oligos CC the IFN-alpha and -beta receptor (030533), was incubated with oligos CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC IFN in the same way as antibodies so are immunosuppressants e.g. for CC toxic side-effects of known immunosuppressants such as steroids.

Sequence 436 AA.
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(EUBI-) LAB EURO BIOTECHNOLOGIE.
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TOVEY M. TIES C.
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WPI; 92-382110/46.
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es 436; Conservative
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                       3IYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                             NONYVLKWDYTYANWTFQVOWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
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Pred. No. 2.3e-203;
% Mismatches 0;
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A (CNRS ) CNRS CENT NAT RECH SCI.

MOGENSEN KE, UZE G, Lutfalla G, G,

N-ESSD; 011701.

New human
                                                                                                                                                                                                                                                                                                                                                                                                   New human alpha interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis Disclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, between residues 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
                                    301
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02-MAY-1991.
19-OCT-1990;
20-OCT-1989;
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R11958;
18-JUL-1991
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Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
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VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                        GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                       GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                         NQNYVLKWDYTYANNTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
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Pred. No. 3.3e-203;
Mismatches 0;
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Matches 436;
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Eid P. Gresser I. Lutfalla G
Tovey MG, Uze G;
WPI; 91-319778/44.
N-PSDB; Q14240.
                                                                                                                                                                                                                                                                                                                                                            aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
Disclosure; Page 47; 52pp; French.
The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R14488;
16-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behoet's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                    GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
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                                                                               NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
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                        GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
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DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

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Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; S8pp; English.

Claim 3; Fig 2; Sepp; English.

Claim 3; Fig
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(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P, Gresser I, Lutfalla G, Me
TOVEY M, UZE G;
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29-OCT-1992.
17-APR-1991; F00318
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                                                                                                                                                                                                                                                                                                                   NQNYVLKWDYTYANMTSQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
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                                                                                                                 GIYLLRYQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIXIGAPKQSGNTP
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Pred. No. 3.3e-203;
; Mismatches 0;
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Best Loc
Matches
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Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation, allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; feminodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody to human interferon type-I receptor -
neutralising activity against human type I interferon, use
therapy and diagnosis
therapy and diagnosis
Disclosure; Fig 3; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benoit P, Maguire
WPI; 93-312951/40.
P-PSDB; R42635.
                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
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Benoit P, Maguire D, Meyer F, Plavec I,
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31-MAR-1992;
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R42635;
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Local Similarity 100.0%;
nes 436; Conservative 0
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            VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                          GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                          GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                         ENTYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
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/label-
/note- "
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"soluble, immunogenic
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Pred. No. 3.3e-203;
; Mismatches 0;
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Best Local Similarity
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16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The amino acid sequence of human interferon class I receptor is given in R73356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monocional antibodies.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as immuno:modulator, eq
Disclosure; Fig.3A-2B; 105pp;
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IFN receptor; inter
interferon-beta; mc
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                                                                                                                         GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTP
                                                                                                                                                          NONYVLKWDYTYANMTFOVQWLHAFLKRNPGNHLYKWKOIPDCENVKTTOCVFPONVFOK
                                                                                                                                                                                                         MYVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                    FSDAVCEKTKPGNTSK
                                    FSDAVCEKTKPGNTSK 436
                                                                            VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
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                                                                VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
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a; monoclonal antibody; immunomodulator;
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/label=
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1. .436
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op; English.
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Pred. No. 7
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7.7e-203;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian soluble interferon alpha-receptor forms used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 7: 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms I (W21805) and 2 (W21805) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
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W21804;
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Transmembranal interferon alpha-receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abramovich C, Ratovitski E, WPI; 95-200634/27.
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(YEDA ) YEDA RES 6 DEV CO
(ABRA/) ABRAMOVICH C.
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                                                                                                                                                                                 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERI 180
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                                                                                     NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                           FSDAVCEKTKPGNTSK 436
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FSDAVCEKTKPGNTSK
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/label- Transmembrane_domain 458. .557
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Pred. No. 9.5e-203;
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RESULT W21805

OSTEDACE

W21805 standard; Protein; 434 AA. W21805; 23-SEP-1997 (first entry) Spliced-deleted interferon alpha-receptor Interferon alpha-receptor; IFNAR. Homo sapiens.

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16-SEP-1994;
17-SEP-1993;
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Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English.

A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coli or COS cell hosts. The protein was used to raise immunomodulatory monoclonal antibodies.

Sequence 436 AA;
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17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
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R71723;
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interferon-beta; monoclonal antibody; immunomodulato
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IFN receptor; interferon receptor;
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181 ENIYSRHKIYKLSPETTYCLKVKAALLISWKIGVYSPVHCIKTTVENELPPPENIEVSVQ 240
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                         FSDAVCEKTKPGNTSK 436
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FSDAVCEKTKPGNTSK
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Pred. No. 1.5e-202;
3; Mismatches 0;
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Example 2: Fig 7: 46pp; English.

Novel splice-deleted interferon alpha-receptor (IFNAR) form 1

(W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal irNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd.

Sequence is predicted from a cDNA clone (see also T73520) obtd.

If from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, to secure and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abramovich C, Ratovitski E, Rever H,
Abramovich C, Ratovitski E, Rever H,
WPI; 95-200634/27.

WPI: 95-200634/27.

New mammalian soluble interferon alpha-receptor forms
New mammalian soluble interferon alpha-receptor forms
  W21806
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domain
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20-OCT-1994; 075977
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                                                                                    VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
standard;
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/note- "comprises amino acid 
transmembranal IFNAR"
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/label= S_domain
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1. .427
Protein;
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496
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Pred. No. 1.6e
0; Mismatches
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..6e-198;
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Novel splice-deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a clone (see also 773521) obtd. Intracellular domain. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed activities of IFNS alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
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Best Local Similarity 97.9%;
Matches 418; Conservative
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20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
(ADRA/) ABRAMOVICH C.
Abramovich C. Ratovitski E. Revel M;
WPI; 95-200634/27.
New mammalian soluble interferon alpha-receptor for New mammalian soluble interferon alpha-receptor for New mammalian soluble interferon alpha-receptor for New mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interferon alpha-receptor for New Mammalian soluble interfer
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23-SEP-1997 (first entry)
Spliced-deleted interferon
Interferon alpha-receptor;
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VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDE------
                                                                                                                                                         NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2208; DB 1;
Pred. No. 1.1e-193;
0; Mismatches 1;
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PS Claim 2; Page -; 79pp; English.

CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1) CC encoding the interleukin-10 (II-10) receptor (IIIOR) and a sequence (S2) cc encoding CRFB4, both operably linked to expression control sequences. CC Cells containing (I) may be used to identify agonists/antagonist of CC II-10. Agonists are potentially useful, e.g. for preventing allograft crejection, as vaccine adjuvants, for treatment of photosensitivity, CC inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, CC viruses, bacteria and parasites (especially intracellular pathogens) and CC restore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a companie of control of a contivity in cells. Antibodies specific for CRFB4 are used to contain the control of contivity in cells. Antibodies specific for CRFB4 are used to contain the control of contivity in cells. Antibodies specific for CRFB4 are used to contain the control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of contr
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CRFB4: interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease; vaccine; photosensitivity; organ rejection; gene therapy.
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(UYNE-) UNIV NEW JERS
Kotenko SV, Pestka S;
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                                                                                                                                                                                                                                                                                                                                                                                            WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                                                                                             HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP 230
                                                                                                                                                                                                                                                                                                                                     NWIKLSGCQNITSTKCNESSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                           WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD
                                                                            EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                                   PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                                                                                       YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                 PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
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l Similarity 29.9%;
67; Conservative 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 AA;
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NEW JERSEY.
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; Pred. No. 5.1e-13;
42; Mismatches 96;
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The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be used to treat pathological conditions associated with endogenous IFN-gamma production.

Sequence 332 AA;
                                                                              agonist; cer.
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(BOEH/) BOEHNI R.
(HEMM/) HEMMI S.
Aguet M, Boehni R,
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                                                                                                                                  Zcytor7 cytokine receptor polypeptide. Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas; Zcytor7; cytokine receptor family; CRF2; prostate tissue; nervous tissue; type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue; agonist; cell proliferation; cell differentiation; renal disease; human;
                                                                                                                                                                                                                                                                               W79159 standard;
W79159;
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09-DEC-1993; US-164596.
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Interferon-gamma receptor beta s
                                                                                                                                                                                                                                                  20-NOV-1998 (first entry)
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WPI; 95-224321/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENVTVGPPKNISVTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                              GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Conservative
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                                                                                                          pancreatic
                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 203; DB 1;
30.1%; Pred. No. 1.1e-10;
tive 38; Mismatches 86;
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.332
  "extracellular
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(ligand-binding) domain;
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RESULT 15
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AC R71035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT Novel human Zcytor? DNA encodes a type 2 cytokine receptor - useful PT for treating renal, neural, pancreatic and prostatic diseases PS Claim 1; Pages 55-59; 72pp; English.

CC This represents the Zcytor? cytokine receptor. Zcytor? is a ligand-
CC binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CRF2). An expression vector containing the Zcytor CC polynucleotide, operably linked to transcription promoter, a sequence CC encoding a transmembrane and intracellular domain, or both, and a CC transcriptional terminator can be used to transform host cells for the CC encoding a transmembrane and intracellular domain, or both, and a CC encoding a transmembrane and intracellular domain, or both, and a CC encoding a transmembrane and intracellular domain, or both, and a CC encoding a transmembrane and intracellular domain, or both, and a CC excombinant production of the polypeptide. The sequences can be used to Study the Zcytor? gene and to isolate ligands binding to it Zcytor? is combinant production of the polypeptide. The sequences can be used to Stimulate proliferation and CC differentially expressed in the Kidney, pancreas, prostate or nervous can be used to Stimulate proliferation and CC differentiation of cell in these organs. The antagonists and agonists can also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
 R71035 standard; Protein; R71035;
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02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
(ZYMO ) ZYMOGENETICS INC.
Addams RL, Farrah TM, Jelmberg AC, Kho
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27-AUG-199A
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                                                                                                               SRTIPPDKTVIEY 401
                                                                                                                                                                                                                    RSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                    --TVPNLKPLTVY
                                                                                                                                                                                  SSLND-----PQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESL
                                                                                                                                                                                                                                                            ------LIYGNEFDKRFFV----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV
                                                                                                                                                                                                                                                                                               CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNI 339
                                                                                                                                                                                                                                                                                                                                     IFWYVLP----ISITV------FLFSVMGYSIYRYIHVGKEKHPANLI------
                                                                                                                                                                                                                                                                                                                                                                         ----LPPPENIEVSVQNQNYVLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPD
                                                                                                                                                                                                                                                                                                                                                                                                              QCVTN----HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIGPPEVALTIDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
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                                                                                                                                                  402
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21.0%; Pred. No. 7e-10;
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                   337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
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Best Local S
Matches 67
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20-AUG-1993; US-110119.
20-AUG-1993; US-110119.
(UYNE-) UNIV NEW JERSEY.
COOK JR, Donnely RJ, Em
COOK JR, SCHWARTZ B, SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suppressing tumours in mammals with accessory factor 1 (AF-1) for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1 DNA in gene therapy Disclosure; Fig 21A; 114pp; English.

The sequence is that of human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant cells. Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9505847-A.
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N-PSDB; Q84697.
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           233
                                                                                   219
                                                                                                                                                        175
                                                                                                                                                                                                                                                                                              120 GALHSAWVTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LLLLLGVFAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYYQVQFK 68
                                                                                                                                                YYVHYWE--KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                                                                                                                                                     YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                           YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL 119
SCYETMADASTELQQVILISVGTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
                                                                        HCIKTTVENELPPPENIEVSV-------QNQNYVLKWDYTYANMTFQVQ 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                      ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
67; Conserv
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22.3%;
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Pred. No. 2.6e-06;
4; Mismatches 112;
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                                                                                                                                                232
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14;

Search completed: June 1, 2000, 04:40:21 Job time: 1344 sec

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Post-processing: Minimum Match 0%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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490.5
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4: /cgn2_6/ptodata/
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Gapop 10.0 , Gapext 0.5
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2313
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(without alignments)
493.702 Million cell updates/sec
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5COMB.pep:*
/cgn2_6/ptodata/1/1aa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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US-08-471-453-2

US-08-37-588-4

US-08-328-256-11

US-08-328-256-12

PCT-US94-14277-3

PCT-US94-14277-4

US-08-683-743-4

PCT-US94-14277-2
US-08-943-087-14
US-08-943-087-18
US-08-943-087-18
US-08-943-087-20
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US-08-328-256-10
US-08-471-454-2
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ALIGNMENTS

## SEQUENCE CHARACTERISTICS: LENGTH: 436 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-307-588-2 RESULT 1 US-08-307-588-2 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIAN Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/307,588 FILLING DATE: 05-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/EP93/00770 FILLING DATE: 30-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 92400902.0 FILLING DATE: 30-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: SAXE, BEINHARD REGISTRATION UMBER: 28,665 REFERENCE/DOCKET NUMBER: 17283/117/GUPL TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 GENERAL INFORMATION: APPLICANT: BENGTI; APPLICANT: MEYER, I APPLICANT: MAGUIRE APPLICANT: PLAYEC, Patent No. Sequence Query Match Best Local Similarity TELEFAX: (202)672-5399 INFORMATION FOR SEQ ID NO: CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 APPLICANT: TOVEY, Michael G. TITLE OF INVENTION: MCNOCCLONAL ANTIBODIES AGAINST THE INTERFERON TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I TITLE OF INVENTION: INTERFERON NUMBER OF SEQUENCES: 4 ADDRESSEE: Foley STREET: 3000 K S CITY: Washington STATE: D.C. ZIP: 20007 Application US/08307588 436 amino acids MAGUIRE, Deborah PLAVEC, Ivan TOVEY, Michael G. BENOIT, Patrick MEYER, Francois 100.0%; <u>ب</u> Score 2313; DB 2; Pred. No. 1.8e-230; Length 436;

Length Indels

557; 0

Gaps

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US-08-328-256-10
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: IL 107378
FILING DATE: 24-OCT-193
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REVEL=13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 248637-37-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08328256 Patent No. 5643749
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    STREET: 419 Seven
CITY: Washington
STATE: D.C.
                         TELEFAX:
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419 Seventh Street, N.W.,
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           SEQ ID NO:
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LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08471454 Patent No. 5731169
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTEALLA, Georges
APPLICANT: GRESSER, Ion
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Best Local (
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN NUMBER OF SEQUENCES: 2
                                                                                        ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A.
ZIP: 22201-4714
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Pred. No. 2.7e-230;
Mismatches 0;
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FOR

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

US 07/900,642

DATE:

06-JUN-1995

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FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                  Sequence 2, Application Patent No. 5861258
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
APPLICANT: MOGENSEN, Knud E. APPLICANT: UZE, G111es
APPLICANT: LUTFALLA, GEORGES
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGM
TITLE OF INVENTION: THE ALPHA
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LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
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                                                                                                                                                                                                                                                      FSDAVCEKTKPGNTSK 436
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                                                                                                                                                                                                                                                                                                                                                                                                                           NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
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                                                                                                                                                                                                                       FSDAVCEKTKPGNTSK 436
                                                                                                                                     Application US/08466974
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 CDNA FRAGMENT CODING THE ALPHA INTERFERON
 FOR THE GENE
RECEPTOR AND
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TOPOLOGY: 1:
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Best Local Similarity
Matches 436; Conserv
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CRASSIFICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REALEST OF THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXU UR
INFORMATION FOR SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PF NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                        181
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                                                                                                                                     241
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STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
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                                                                GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
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                              VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
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22201-4714
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1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                Query Match 100.0%; Score 2313; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-230; Matches 436; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-TUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-TUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-TUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGITERATION NUMBER: ER 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGITERATION NUMBER: ER 89/13770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXU UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALDHA INTERFERON RECEPTOR AND PROCESS PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 NORT
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LUTFALLA, Gec
APPLICANT: GRESSER, Ion
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             121
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                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 557 amino acids TYPE: amino acid
                                                                                                                                                              ADDRESSEE:
                            TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                     FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
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; MOLECULE TYPE: US-08-307-588-4
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                              TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Patent No.
                                                                                                                                          REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/1
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                       NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 NQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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3000 K Street; N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEYER, Francois
                protein
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Query Match Best Local Similarity

100.0%;

Score 2313; DB 2; Pred. No. 2.7e-230;

Length 557;

Mismatches

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Indels

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SEQUENCE CHARACTERISTICS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,2:

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION UMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ABRAMOVICH, Carolin APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                      STREET: 419 Seven CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ب
                                                                    NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
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             248633
FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                          USA
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; MOLECULE TYPE: protein US-08-328-256-11
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US-08-328-256-12
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Best Local Similarity
Matches 427; Conserv
                                                                                                                                                                                                                                              Sequence 12, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
         ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION UNMBER: US/08/328,256

FILING DATE: 24-OCT-1994
                                                                                                                                                                                 NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                     APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                  421 FSDAVCE 427
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                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
CITY: Washington
STATE: D.C.
COUNTRY: USA
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Pred. No. 1.6e-225;
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                                                     #1.30
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APPLICATION NUMBER:

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PCT-US94-14277-3
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                                                                                                                                                                                                                                        Sequence 3, Application PC/TUS9414277 GENERAL INFORMATION:
                                        APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 419;
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Best Local Similarity
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           414 -SDAVCE 419
                                                                                                                                                                                                                                                                                                                                                                             421 FSDAVCE 427
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361 VIODYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTNDE------ 414
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TELEFAX: 202-737-3528
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NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: REVI
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                            COUNTRY:
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MYVYLLGATTLYLVAVGFWYLSAAAGGKNLKSDOKVEVDIIDDNFILRWNRSDESYGNYT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
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            94080
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24-OCT-1993
                                                                                                                                                         Receptor Subunit Polypeptides
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PCT-US94-14277-4
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtin (Genentech) CURRENT APPLICATION NUMBER: PCT/US94/14:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                    TITLE OF INVENTION: Receptor Subunit Polypeptides NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Aguet, Michel APPLICANT: Bohni, Ruth APPLICANT: Hemmi, Silvio
                                                                                                                                                                           STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                               COUNTRY: UZIP: 94080
                                                                                                                                                                                                                                            ADDRESSEE:
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В Ş B Ş 밁 S В δõ 밁 Š

USA

360 Kb floppy disk

Hemmi, Silvio

Genentech,

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PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 antino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/164

FILING DATE: 09-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
181 PSLKKHSNYSTXQCISTTVANK 202
                                                                                                         147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                       207 LTSWKIGVYSPVHCIKTTVENE 228
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                                                                                                                                                 61 EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                                    88 NFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible operating system: pc-Dos/MS-Dos SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/14277 FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                    SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                                                                                                                                                                                                                                ch 21.2%; Score 490.5; DB 4 1 Similarity 48.5%; Pred. No. 7.4e-43; 98; Conservative 34; Mismatches 69
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Gaps 87

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CLASSIFICATION: IOR APPLICATION DATA:

APPLICATION NUMBER:

08/164596

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Best Local Similarity
"~* hes 93; Conserve
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                                          APPLICATION NUMBER: US/08
FILING DATE: 17-UUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,6
                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pestka, Sidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 LPPPENIEVSVQNQNYVLKWDY-TYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 V-LFRALLNKTSNFSEKLCEKTRPGSFS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 IYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKAR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 TTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFH 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 601
                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANVQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICANT: KOLENKO, SERGUE1

E OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYXNCQDSTCD-----GLNYEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHTMDEKLNKSSVFSDAVCEKTKPGNTS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTHCVFSQDTXYTGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTLL 120
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                                                                                                                                                                                                                                                                                                                        New Jersey
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44.7%; Pred. No. 2.2e-40;
                                                                                                                             US/08/683,743
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Best Local :
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LENGTH: 325 amino acids
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                                                                                                          131 PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
176 EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP 219
                                  187 HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP 230
                                                                                                                                                                                                                                                                                    9.9%;
Local Similarity 29.9%;
les 67; Conservation
                                                                                                                                            59 YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                                                                                                                                                72 WWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                        19 WYLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
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                                                                                                                                                                                                                    3 WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                                    PGMQVEVLADSLHMRFLAPKIENEYETWTMKNYYNSWTYNVQYWKNGTDEKFQITPQYDF 175
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                                                                                                                                                                                                                                                                                                             Score 228.5; DB 7
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                Length
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Gaps

PCT-US94-14277-2 Sequence 2, Application: TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
FILING DATE: 07-DEC-199
CLASSIFICATION: COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: Love, Richard B. PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 09-DEC-) CORRESPONDENCE ADDRESS VE INVENTION: Receptor Subunit Polypeptides COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) TELEFAX: TELEPHONE: COUNTRY: NSSEE: Genentech, Inc.
T: 460 Point San Bruno
South San Francisco
California 94080 Application PC/TUS9414277 USA Hemmi, Silvio Aguet, Michel Bohni, Ruth 09-DEC-1993 07-DEC-1994 08/164596 PCT/US94/14277 866PCT

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PCT-US94-14277-2
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                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1. Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
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                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 98102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                               amino acid
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Adams, Robyn L.
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Kho, Choon J.
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01 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                Paul G
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                          single
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30.1%; Pred. No. 8e-13;
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Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, App.
                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                               STREET: Seattle
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 SRTIPPDKTVIEY 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI----QAFLLPPVFNI 339
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                                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
                                                      APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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Similarity 21.0%;
                                                                                                                                                                                                                                                                                                                                           INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                          Kho, Choon J.
                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                  Farrah, Theresa M. VENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                     Jelmberg, Anna C.
Adams, Robyn L.
Whitmore, Theodor
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                                                                                                                                         IBM Compatible
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internal
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                                                                      US/08/943,087
08/803,305
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Pred. No. 6e-12;
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US-08-943-087-16
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                                                                                                                                                                                                                                         Sequence 16, Application US/08943087 Patent No. 5945511
                                                     APPLICANT: Lok, S1
APPLICANT: Kho, Choon J.
APPLICANT: Jehnberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
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SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                  GENERAL INFORMATION:
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REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                     CORRESPONDENCE ADDRESS
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TYPE: amino acid
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                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------LIYGNEFDKRFFV----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE------
2: ZymoGenetics, Inc.
1201 Eastlake Avenue East
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Best Local Similarity
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8.6%; Score 198; DB 2 21.0%; Pred. No. 6e-12;

DB 2; Length 553;

17;

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TELEX:
INFORMATION FOR SEQ ID NO:
TOPOLOGY: 11
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                 REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 98102
                                                 LENGTH: 553 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/803,305 FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/943,087
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                                     linear
 protein
internal
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136 QIGPPEVALITDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195 340 RSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV 391 178 ERIENIYSRHKIYK--LSPETTYCLKYKAALLTSWKIGYYSPVHCIKTTVENE-----389 SRTIPPDKTVIEY 401 392 -- TVPNLKPLTVY 402 11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67 76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135 68 TGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI -- - QAFLLPPVFNI 339 SSLND-------LIYGNEFDKRFFY----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV 336 IFWYVLP----ISITV------FLFSVMGYSIYRYIHVGKEKHPANLI-----------LPPPENIEVSVQNQNYVLKWDYTYANWTFQV-QWLHAFLKRNPGNHLYKWKQIPD 282 QCVTN----HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKI 251 Conservative -----PQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESL 79; Mismatches 173; Indels 90; Gaps 388 229 290

Search completed: June 1, 2000, 05:52:41 Job time: 4640 sec

Title: Perfect score: Sequence:

US-09-240-675-2 2313 1 MMYVLLGATTLVLV

Scoring table:

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Post-processing: Minimum Match 0%
Listing first 45.summaries
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Gapop 10.0 , Gapext 0.5
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frazzled gene prot
neogenin - chicken
190K protein - hum
                                                                                                                                                                                                                                            interleukin-10 rec
tumor suppressor -
probable protein-t
titin, muscle - ch
                                                                                                                                                                                                                                                                                                                                           insulin receptor p
interferon gamma r
receptor-like tyro
receptor tyrosine
                                                                       protein-tyrosine-p
protein-tyrosine-p
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interferon alpha r
interferon alpha/b
hypothetical prote
twitchin - Caenorh
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                                                                                                                      protein-tyrosine k
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                                                                                                                                               titin, cardiac mus
                                                leukocyte antigen:
                                                                                                                                                                 nypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interferon recepto
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R;Lutfalla, G.

R;Data Library, July 1991

A;Description: The structuree of the human interferon alpha/beta receptor gene.

A;Reference number: S17112

A;Accession: S17112

A;Accession: S17112

A;Rolecule type: DNA

A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross_references: EMBL:X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: GDB:IFNAR; IFRC
A;Gene: GDB:IENAR; IFRC
A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21922.1-21922.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; 9lycoprotein; transmembrane protein
F;1-21/Domain: transmembrane #status predicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon alpha/beta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C;Accession: A33694; S17112
R;Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into A;Reference number: A32694; MUID:90124632
A;Accession: A32694; MUID:90124632
A;Accession: A32694
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A;Residues: 1-557 <UZE>
A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 436; Conservative
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                    ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ 240
                                                                                                                                               TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                  MMVVLLGATTLVLVAVGÞWVLSAAAGGKNLKSÞQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                       FSFDYOKTGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                         MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
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991
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878
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1825
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100.0%; Pred. No. 3.2e-165;
tive 0; Mismatches 0;
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1700348
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A40091
S51603
T32828
S41602
T16580
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receptor-like tyro
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interferon alpha r
hypothetical prote
IL12 receptor comp
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Result No.

Query Match

Length

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Gaps

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Database :

PIR\_63:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Minimum DB Maximum DB

seq length: 0 seq length: 1000000

Searched

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C:Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett 313, 255-259, 1992
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A; Residues: 1-421, 'V', 423-560 <LIM>
A; Cross-references: EMBL: 106320; NID: 9163187; PIDN: AAA02571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha
A;Reference number: S33770; MUID:93305725
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                                                                                                                                                                                                                                                                                                 B
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F;25-560/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: lung C: Keywords: antiviral; cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-560 <MOU>
A; Cross-references: EMBL: X68443; NID: g431; PIDN: CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Specific antiviral activities of A; Reference number: S27387; MUID:93076908 A; Accession: S27387
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A;Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon alpha receptor type 1 precursor - bovine
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Best Local
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   299
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                                                                                                                                                               FTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEE 178
                                                                                                                                                                                                                                 VQNQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVF
                                                                                               RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKVPSPENIQIN
                                                                                                                                                                                                                                                                                                                                  MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
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QKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLS-DSFHIYIGAPKQSG
                                                                                                                                RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVS 238
                                                                                                                                                                                                                                                                                                   MLALLGATTLMLVA-GRWVLPAASGEANLK-PENVEIHIIDDNFFLKWNSSSESVKNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONYVLKWDYTYANMTFOVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                  65.2%; Score 1507; DB 2; 64.9%; Pred. No. 5.2e-105; Live 65; Mismatches 83;
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                        A;Gene: IFNAR
A;Introns: 177/3; 331/1
C;Keywords: cytokine receptor; transmembrane protein
                                                                              A;Cross-references:
C;Genetics:
                                                                                                             A; Molecule type: DNA
A; Residues: 473-590
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 426-445
                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 265-375 <RE4>
A;Cress-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1;
A;Accession: I48427
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                                                                                                                                                               A; Accession: I48429
                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                              A; Status: preliminary; translated
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A; Accession: I48428
                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 397-424 < RE5>
                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; A;Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 118-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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                                                                                                                                            preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-590 <UZE>
                                                                                                                                DNA
                                                                                                                                                                                                                  DNA
                                                                                             <RE7>
EMBL:U06244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <RES>
EMBL:U06237; NID:g497103; FIDN:AAA65003.1;
                                                                                                                                                                                                                                                               EMBL: U06241;
                                                                                                                                                                                                  <RE6>
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C;Species: Mus musculus (house mouse)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A45289; 148423; I48424; I48425; I48426; I48427; I48428; I48429
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NMSVNQLYPLIYEVIFWENTSNAERKVLEKRINFIFPDLKPLTVYCVKARALIENDRRNK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNK 417
          expressed
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R;Lutfalla, G.; Uze, G. Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high A;Reference number: I48423; MUID:95047447
A;Accession: I48423 A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; A;Note: sequence extracted from NCBI backbone (NCBIN:102354, PID: 9194112 NCBIP: 102357)

Status: preliminary; translated from GB/EMBL/DDB.

Status: preliminary; translated from GB/EMBL/DDBJ PID:g755811 PID: 9755810

Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; A;Accession: 148426 PID:g510261

GB/EMBL/DDBJ PID:g510262

NID: 9497110; PIDN: AAA65006.1; from GB/EMBL/DDBJ PID:g755812

EMBL: U06242; NID: g497112; PIDN: AAA65007.1; PID: g755813 translated from GB/EMBL/DDBJ

NID: g497114; PIDN: AAA65008.1; PID:g510265

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cytokine receptor family II, member 4 - human cyspecies: Romo sapiens (man) C:Date: 21-Dec-1996 *sequence_revision 06-Jun-1997 C:Accession: G01418 R:Lutfalla, G. submitted to the EMBL Data Library, April 1994 A:Reference number: G06935
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A;Cross-references: GDB:138168; OMIM:123889
A:Map postition: 21922.1-21922.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
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                                                                                                                                                                                                                                Query Match
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Best Local Similarity
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                                 131
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                                                                59
                                                                                               72
                                                                                                                                                               19 WYLSAAAGGKNLKS------PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                Local Similarity 29.9 es 67; Conservative
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PGMQVEVLDDSLHMRFLAPKIENEYETWIMKNVYNSWIYNVQYWKNGTDEKFQITPQYDF
                             PEVHLEAEDKAIVIH-ISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                              YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                             NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GLNYEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNT
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                                                                                                                                                                                                            10.18; 29.98;
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                                                                                                                                                                                                44;
                                                                                                                                                                                             Score 233.5; DB 2;
Pred. No. 2.6e-10;
Prematches 94;
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C;Accession: A47003
R;Lutfâlla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene
A;Reference number: A47003; MUID:93300510
A;Accession: A47003
                                                                                                                                                                                                                             A; Reference number: JC6311
A; Accession: JC6311
A; Status: preliminary
                                                                                                                                                                                                                                                                               C; Accession: JC6311
R; Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A; Title: CRF2-4:isolation
                                                                                                                                                                                                                                                                                                                                           interferon receptor-class II cytokine receptor -
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-19:
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C; Keywords: transmer
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A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine receptor family class II protein CRF2-4 precursor C; Species: Homo sapiens (man)
C; Date: 09-Sep-1994 *sequence_revision 09-Sep-1994 *text_ch
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A; Residues: 1-349 <GIB>
A; Cross-references: GB:
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Best Local (
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                                                                                                  Matches
                                                                                                            Query Match
Best Local Similarity
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                                                              16 VGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNW 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAOIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
IKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPE 132
                                LGGFLLVPALG--MIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP
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67; Conservative
                                                                                               Conservative
                                                                                                                                                                                 GB:U53696
                                                                                                              9.6%;
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                                                                                                                                                                                                                                                                                 of cDNA clones encoding the
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                                                                                                  49;
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Pred. No. 7.8e-10;
                                                                                                              Score 221.5;
Pred. No. 2.1
                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID: g393379
                                                                                                              .9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                 mouse
                                                                                                                                                                                                                                                                                                                                                #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 10-sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family maps
                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
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                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                               Length 349;
                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                  29;
                                                                                                                                                                                                                                                                                    mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                    10;
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interferon gamma receptor beta subunit - mouse
N.Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
R:Hemmi, S: Bohni, R: Stark, G:; Di Marco, F:; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionalit
A:Reference number: A49947; MUID:94170381
A:Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note:
C; Keywor
                                                                                                                                                                                                                             interferon gamma receptor accessory factor-1 precursor - human
c;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-332 <AEN>
A;Rosidues: 1-332 <AEN>
A;Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
                                                                                                                                                    Cell 76, 793-802, 1994
A:Title: Identification and
A:Reference number: A49946;
A:Accession: I38500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ş
                       A; Residues:
                                         A; Molecule type: mRNA
                                                             A; Experimental A; Accession: I:
                                                                                                                A; Molecule type: mRNA
A; Residues: 1-337 < RES>
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                                                                                            A;Cross-references: EMBL:U05875; NID:g463549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                        185
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                                                                                                                                                                                                             J.; Donnelly, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                          NIYSRHKIY -- KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSAAAGG----KNLKSPOKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYOKTGM
                                                                                                                                                                                                                                                                                                                                                                                                  GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHLEAEDKAIVIHIS-----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YENVTVGPPKNISVTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDSEVLRNLEPWTTYCIQVQGFLLDQNRTGEWSEPIC-ERTGNDEITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQIESLAESLELRFSAPQIENEPET-----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
1-63,'Q',65-337 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine receptor
                                                           al source: clone pSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CKRTASTQCDFS--HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8%;
                                                                                                                                                                       sequence of an accessory factor required for activation of \mbox{\sc MUID}\xspace: 94170380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
   NID:g463551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 203; DB
Pred. No. 6.5e-
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor family complements functionality
 PIDN: AAA16956.1;
                                                                                              PIDN: AAA16955.1;
                                                                                                                                                                                                                             T.M.; Cook, J.R.; Wang, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08;
                                                                                                                                                                                                                                                                  #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                    233
 PID:g463552
                                                                                            PID: 9463550
                                                                                                                                                                                                                                                                  05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                             Emanuel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Drosophila melanogaster
C;Date: 20-Sep:1999 *sequence_revision 20-
C;Accession: T13822
R;Kolodziej, P.A.; Timpe, L.; Mitchell, K.
Cell 87, 197-204, 1996
A;Title: Frazzled encodes a Drosophila mer
A;Reterence number: 217780
A;Accession: T13822
A;Accession: T13822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone | C; Genetics:
A; Map position: 21
C; Keywords: cytokine receptor
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                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: may
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C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-1375 < KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frazzled gene protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
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Best Local Similarity 22.3
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                       Matches 102;
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated
                                                                                                                                  104
                                                                                                                                                                                                                                                  447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                    26 GGKNLKS------PQKVEVDIIDDNFI-LRW-------NRSDESV 56
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                  -- IRAEKENTSSWYE----
                                                                                                                                                                                                         GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCIKTTVENELPPPENIEVSV---
                   ISVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQI
                                                           DSFTPFRKAQIG----
                                                                                            GYARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYV 626
                                                                                                                                                                     KMVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFE 566
                                                                                                                                                                                                                                                GGKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQ 506
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    function in vivo as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:U71001;
                                                                                                                                                                                                                                                                                                                                           16.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%; Score 155.5; DB 2; 22.3%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pJS3
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                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g1621114; PID:g1621115;
                                                                                                                                                                                                                                                                                                                                           Score 129; DB Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                       Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.J.; Goodman, C.S.; Fried,
                                                         PPEVHLE-AEDKAIVIHISPGTKDSVMWAL
                                                                                                                                                                                                                                                                                                                                                                                                                    receptor or
                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                             Length 1375;
                                                                                                                                                                                                                                                                                                                                                                                                                    component
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: AAC47314.1
                                                                                                                                                                                                                                                                                                                         268;
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20-Sep-1999

S.; Jan,

L.Y.;

subfamily

of a

receptor mediat

Gaps

22;

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686

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120 GALHSAWYTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 VLVAVGPWVLSAAAGG----KNLKSPQKVEVDIIDDNFILRW------NRSDESVGNVTFS
                                                                                                                            YYVHYWE--KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                                                                                                                           YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                             FDYOKTGMDNWIKLS------GCONITSTKCNFSS------LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK 68
SCYETMADASTELQQVILISVGTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
                                                                                                                                                                                                                                                                                                                       ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                                                                                      YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL
                                                                 -QNQNYVLKWDYTYANMTFQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
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                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                 260
                                                                                                                               232
                                                                                                                                                                                                                                                            174
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OY 355 OSGNTPVIQDYPLIYBIIFWENTSNAER-KIIEKKTDVTVPNL	Db 838 TGYKIRYRKFKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEMNR 894		
Qy 303YLLRVQASDGNUTSFWSEEIKFDTEIQAFLLPPVF	778 ISVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQI 8		
Qy 253 ANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQ			
QY 194 PETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIE	ONVIES FUND   COMMUNICATION	QY 138 EDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGV	
Qy 78 GCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF	Best Local Similarity 16.4%; Pred. No. 0.18; Matches 102; Conservative 68; Mismatches 184; Indels		
Qy 21 LSAAAGGKNLKSPQKVEVDIIDDNFI-LRWNRSDESVGNVT  :	<pre>Map position: 2 Query Match 5.6%; Score 129;</pre>		
Query Match 5.5%; Score 127.5; DB 2; Best Local Similarity 22.2%; Pred. No. 0.21; Matches 92; Conservative 61; Mismatches 201;	A;Residues: 1-1526 <kol> A;Cross-references: EMBL:U71002; NID:g1621116; PID:g1621117; PIDN:AAC47315.1 C;Genetics: A;Gene: frazzled</kol>		
A;Cross-references: EMBL:U07644; NID:g641965; PID:g64	A;Accession: T13823 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA		
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1443 <vie></vie>	996 ncodes a Drosophila member of the DCC immunoglobulin subfamily ar 217780		
J. Cell Biol. 127, 2009-2020, 1994 A;Title: Neogenin, an avian cell surface protein expr. A;Reference number: A55193; MUID:95105243 A;Accession: I50600	C:Species: Drosophila melanogaster C;Date: 20-Sep-1999 *sequence_revision 20-Sep-1999 *text_change 20-Sep-1999 C;Accession: T13823 R;Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan,		
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #t C;Accession: I50600 R;Vielmetter, J.; Kayyem, J.F.; Roman, J.M.; Dreyer,	ESULT 10 13823 razzled gene protein		
RESULT II 150600 150600 chicken (fragment) C:Sportes Gallus Gallus (chicken)	Db 1016 TMLMLPNLKPYTTYYFKVQART 1037		
	Qy 389 TDVTVPNLKPLTVYCVKARAHT 410		
QY 389 TDVTVPNLKPLTVYCVKARAHT 410   : :          :   Db 1167 TMLMLPNLKPYTTYYFKVQART 1188	Qy 342 LSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKK 388 : : : :   ::              : : : :  ::		
QY 342 LSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWEN : :   : :	Qy 282 DCENVKTTQCVFFQNVFQKGIYLLRVQASDGNNTSFWSEEIKEDTEIQAFLLPPVFNIRS 341		
QY 282 DCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSEWSEEIKFI	Qy 251TYANMTFQVQWLHAFLKRNPGNHLYKWKQIP 281   ::    :   ::  ::  ::  ::  ::  ::  ::		
Db 1004 APTPLEVPVGLRATMSSSSIVYKWIDTMLNKNOHYTDNRHYT	Db 793 WGRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVD 852		
248 W 1 944 WGRGIPDENTIEL	213 GVYSPVHCIKTIVENELP		
213 GVYSPVHCIKTTVENELP  :  :   :  :  895 ANTLENDLDETQVPGKPI	159 DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKI		

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--PPENIEVSVQNQNYVLK 247
||::|::::!!!|
||GPPQHPEIKI--RNYVLG 943
                                                      KFDTEIQAFLLPPVFNIRS 341
| ; |}
LNSTYQNVPVTPP----- 1111
                                                                                                                 ------PGNHLYKWKQIP 281
|:: |::
YTVSYGITGSNRYRY---- 1060
DTTKRDRDWSVEAFAGEE 1166
                  ENTSNAER-----KIIEKK 388
                                                                                                                                                                             EDGPPIYDNIKTRDEEPVD 1003
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pressed during terminal neuron #text\_change 13-Sep-1996

Length 1443; NLKPLTVYCVKARA 408 -FNIRSLSDSFHIYIGAPK 354
::| | | : | | | |
SLHVRPLVTSI-VVSWTPP 746 GVEERIENIYSRHKIYKLS 193 |: :: : | | DSEQDVDVAGLSYTITGLK 586 SETPERKAQIGPPEVHLEA 137 l; Indels 61; Gaps VTFSFDYQKTGMDNWIKLS 77 ||:| | | | | LTYSIFYTKEG----INRE 471 19;

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A:Title: The globular head domain of titin extends into A;Reference number: S42166; MUID:94095655
A;Accession: S42167
                                                                                                                                                                                                                     insulin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-1990 #sequence_revision 14
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                  Mol. Endocrinol. 4, 235-244, 1990
A;Title: The rat insulin receptor: primary structure
A;Reference number: A36080; MUID:90231337
A;Accession: A36080
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A;Residues: 1-1451 <VIN>
A;Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA48833.1;
A;Cross-references: GB:M29014; NID:g204953; PIDN:AAA41441.1; C;Superfamily: insulin receptor; protein kinase homology
                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1383 <GOL>
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Goldstein, B.J.; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CDITCLESFRDSMVLGWKQPDKTGGAEITGYYVNYREVIDGVPGKWR----EANVKAVREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TCHGLVTGQS----
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91; Conservative
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19.8%;
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Pred. No. 0.42;
7; Mismatches
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C;Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; transmembra F;1022-1298/Domain: protein kinase homology <KIN> F;1030-1038/Region: protein kinase ATP-binding motif
interferon gamma receptor precursor - ]
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision
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                                                                                                                                   KESLVISGLRHFTGYRIELQACNQDSPEERSGV-AAYVSARTMP
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89; Conserv
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Pred. No. 0.86;
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                                       human
 28-Feb-1990 #text_change
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   23-Jul-1999
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A;Gene: GDB:IFNGR1; IFNGR A;Cross-references: GDB:120688; OMIM:107470 A;Map position: 6q23-6q24 C;Superfamily: interferon gamma receptor C;Keywords: cytokine receptor; transmembrane protein R:Aguet, M.: Dembic, Z.; Merlin, Cell 55, 273-280, 1988
A:Title: Molecular cloning and e A:Reference number: A31555; MUID A:Accession: A31555 Š В δÃ C; Genetics: A; Molecule type: mRNA A; Residues: 1-489 < AGU> C; Accession: A31555 A; Cross-references: GB: J03143; NID: g184650; Query Match Best Local ( 227 Local 27 NVKTTQCVFPQNVFQKGIYL-LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS--SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE-----VKNYGVKNSEW--IDACI 78 NELPPPENIEVSVONONYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE 284 l Similarity 50; Conserv 5.1%; Score 118; DB 2; Ilarity 22.2%; Pred. No. 0.25; Conservative 39; Mismatches 10 and expression; MUID:89003065 of. PIDN: AAA52731.1; the 102; human Length 489; Indels interferon-gamma receptor PID: g306915 Gaps 342 10:

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R;Malsonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam A;Reference number: $49015; MUID:94067777
A;Accession: $51604
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor-like tyrosine kinase Ehk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
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A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
C;Keywords: ATP; transmembrane protein
F;653-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif
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                                   374 WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 410
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                                                                                                                                                              360 PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR--- 416
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Search completed: June

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                                                                                  VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTVPNLKPLTYYCVKARAHTMDEKLNKSSV 420
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                                                       FSDAVCEKTKPGNTSK
                                                               FSDAVCEKTKPGNTSK 436
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(Rel. 27, Created) (Rel. 28, Last seq
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                     STANDARD;
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sequence update)
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L -> V.
/FTId-VAR_002717.

G -> A (IN REF. 2)
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Pred. No. 4.4
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INTERFERON-ALPHA/BETA RECEPTOR
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                     PRT;
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OF6744C8A1ADBE73 CRC64;
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4.4e-166;
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TRANSMEM
DOMAIN
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"Cloning and characterization of a boyine alpha interferon receptor.";

"Cloning and characterization of a boyine alpha interferon receptor.";

siochim. Biophys. Acta 1173:314-319(1993).

I Sincinok: Receptor for interferons alpha and Beta. Binding to Type

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBGUNITS THEMSELVES.

SUBGUNITS THEMSELVES.

SUBGULLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBGULLULAR LOCATIONS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SUBGULLARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                            CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                            EMBL; X68443; CAA48484.1; -.
EMBL; L06320; AAA02571.1; -.
PIR; S33770; S33770.
PIR; S27387; S27387.
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouchel-Vielh E., Lutfalla G., Mogensen K.E. "Specific antiviral activities of the human determined at the level of receptor (IFNAR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNAR1 OR IFNAR.
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MEDLINE; 93305725.
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[2]
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                                                                                                                                                                                                                                                                                                 Receptor;
                        Match
                                                                                                                                                                                                                                                                                                 Transmembrane;
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173
1313
3134
434
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                                                               63818
           64.98;
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BY SIMILARITY.
                                                               W.
 Score 1507; D
Pred. No. 1.1e
55; Mismatches
                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                              POTENTIAL.
F -> V (IN REF. 2).
66D76B72861E1D11
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uman alpha interferons
NAR) structure.";
 ; DB 1;
1.1e-105;
hes 83;
                                                               CRC64;
                         Length 560;
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O BETA-
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Local Similarity hes 285; Conserv

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Gaps

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SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKL-NVYEEIKLRIRAEK-ENTSSWYEVDS

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RESULT 3
                                      Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

"Molecular cloning of ovine and bowine type I interferon receptor

graphics from uter1, and endometrial expression of messenger

ribonucleic acid for ovine receptors during the estrous cycle and

pregnancy.";

LE Endocrinology 118:4757-4767(1997).

C. -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

C. -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA-

NOTIONAL TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

C. -!- SUBCLIDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

C. -!- SUBCLIDINAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -!- SUBCLIDIAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -!- SUBCLIDIAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -!- SUBLIBRATIY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

C. -!- SUMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q28589; Q95206;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN
(INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                          Kaluz S., Fisher P.A.,
"Structure of an ovine endometrium.";
J: Mol. Endocrinol. 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; F
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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EMBL; X95939; CAA65183.1; -. EMBL; U65978; AAB84231.1; -. PFAM; PF00041; fn3; 1.
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SSVFSDAVCEKTKPGNTSK 436
                                NTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNK
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                      NMSVNQLYPLVYEVIFWENTSNAERKVLEKRTDFTFPNLKPLTVYCVKARALIENDRWNK
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BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
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A -> D (IN REF 2).
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                                                                                                                                                                                                                                                                                                                                             Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERPRENON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNARI OR IFNAR OR IFAR.
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                          or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
15-FEB-2000 (Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INR1_MOUSE P33896;
                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Behavior of a cloned
  181
                                         121
                                                            61
                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pehavior of a cloned murine interferon alpha/beta receptor i homospecific or heterospecific background."; oc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).

FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDIT I INS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF FUNCULUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND SUBUNITS THEMSELVES.

SUBCELLIFIAD TOWNS.
                                                                                                                                         Local Similarity
les 212; Conserv
                                                                                                 <u>بــ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                       MGI:107658;
                              TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                          SAEYRTKDEAKWLKVPECQHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPF
                                                                  SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSF
                                                                                               MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                  IPFYTAHMSPPEVRLEAEDKAILVHISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTI
                                                                                                                                                                                                                                                                                                                                                                                         M89641;
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
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430
450
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                                                                                                                                         Conservative
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                                                                                                                                                                                        65776
                                                                                                                                                46.2%;
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POTENTIAL.
                                                                                                                                                                                        MΨ;
                                                                                                                                         77;
                                                                                                                                       Score 1069; DB 1;
Pred. No. 7.9e-73;
7; Mismatches 137;
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BY SIMILARITY.
POTENTIAL.
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                                                                                                                                                                                      POTENTIAL.
7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                        Indels
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                                                                                                                                                          590;
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                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A new member of the cytokine receptor gene family maps on chromosome 21 at less than 35 kb from IFNAR."; Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 96054036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                               PIR; A47003; A47003.
HSSP; P13726; 1DAN.
                                                                                                                                                                                                                    EMBL; Z17227; CAA78933.1; -. EMBL; U08988; AAA86872.1; -.
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Q08334;
                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
-I- SUBCELULIAR LOCATION: TYPE I MEMBRANE TOTEIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Evol. 41:338-344(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neighbor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lutfalla G., McInnis M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                 123889
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                                                                                                                                          Transmembrane;
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                                                                                                                                        Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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CYTOKINE RECEPTOR CLASS-II CRF2-4.
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on with
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RESULT 6
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Best Local Similarity
Matches 67; Conser
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
SEQUENCE
             EMBL; U05875; AAA16955
EMBL; U05877; AAA16956
MIM; 147569; -.
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LUNG FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
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Pred. No. 3.5e
2; Mismatches
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VARIANT
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SIGNAL
                                                                                     Vinkemeler U., Obermann W., Weber K., Fuerst D.O.;
"The globular head domain of titin extends into the center of t sarcomeric M band. cDNA cloning, epitope mapping and immunoelec microscopy of two titin-associated proteins.";
J. Cell Sci. 106:319-330(1993).
-i- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS
                                                                                                                                                                                                                                                                                             MYNI HUMAN STANDARD; PRT; 1451 AA.

P52179;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          HUMAN
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                         Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
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                                         -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                              TISSUE-SKELETAL MUSCLE; MEDLINE; 94095665.
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PEAM; PE00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
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                                                                                                 TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                KL-----RIRAEKENTSSW-----YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS
                                                                       A-YKISNLKENMVYQFQVAAMNMAGLGAPSAVSECFKCEE
                                                                                                                                                                                 ---TCHGLVTGQS-----YIFRVRAVNAAGLSEYSQDSE-AIEVKAAIAPPSPP
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                                                                                                                                                     --VFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEII-----FWENTSNAERKIIEKK
                                                                                                                                                                                                                                        PSRNTDTSV-----VVSWEESKDAKELVGYYIEANVAGSGKWEPC--NNNPVKTHRF---
                                                                                                                                                                                                                                                               PPENIEVSVQNQNYVLKWD------YTYANMTFQVQWLHAFLKRNP-GNHLYKWK
                                                                                                                                                                                                                                                                                                                                                  EPSEGIVPGPPTDLSVTEATRSYVVLSWKPPGQRGHEGIMYFVEKCEAGTENWQRVNTEL
                                                                                                                                                                                                                                                                                                                                                                            PGTKDSVMWALDGLSFT----YSLLIWK-----NSSGVEERIENIYS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYIIISWKQPAVDGGSPILGYFIDKCEVGTDSW-----SQCNDTPVKFARFPVT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                        RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTV-----ENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 123.5; DE
Pred. No. 0.19;
67; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; Thick filament; Repeat.
6 X 6 AA TANDEM REPEATS.
    PRT;
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  EMBL; M29014; AAA41441.1; -.

EMBL; AF005775; AAB61415.1; -.

EMBL; U80637; AAB61415.1; -.

EMBL; U80633; AAB389746.1; -.

EMBL; U80633; AAB38968.1; -.

EMBL; U80630; AAB38968.1; -.

EMBL; U80630; AAB38967.1; -.

EMBL; U80630; AAB38967.1; -.

EMBL; U80629; AAB38967.1; -.

EMBL; U80629; AAB38967.1; JOINED.

PIR; A36080; A36080.

HSSP; P06213; IIRK.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00109; TYRKINASE.

PRINTS; PR00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
                                                                                       PROSITE; rbovv...; fn3; 1.

PFAM; PF000069; pkinase; 1.

PFAM; pF000757; Furin-like; 1.

PFAM; pF01030; Recep_L_domain; 1.

PFAM; PF01030; Recep_L_domain; 1.

"ransferase; Tyrosine-protein kinase; Receptor; Tran-
"ransferase; Tyrosine-protein kinase; Receptor; Tran-
TRANSMEM
DOMAIN
DOMAIN
                                        CHAIN
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P15127; P97681;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR).
                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldstein B.J., Dudley A.L.;
"The rat insulin receptor: primary structure and conservation tissue-specific alternative messenger RNA splicing.";
no.1. Endocrinol. 4:235-244(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
MEDLINE: 90231337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu Y., Tam J.W.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN TYROSINE PHOSPHATE.

ENEXME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
ACTIVITY:

SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASES.
  27
761
764
764
958
979
 26
760
763
1383
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957
978
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1383
POTENTIAL.
CYTOPLASMIC (POTENTI,
FIBRONECTIN TYPE-III
                                     INSULIN RECEPTOR, ALPHA
REMOVED IN MATURE FORM
INSULIN RECEPTOR, BETA-
EXTRACELLULAR (POTENTIA
                                                                                                                        Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ong as its content is in
             (POTENTIAL)
                                        (POTENTIAL).
                                                     BETA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP
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Rattus.
                                                                                                            Repeat.
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RESULT 9
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Best Local S
Matches 89
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CARBOHYD
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ACT_SITE
DISULFID
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CONFLICT
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BINDING
INGR_HUMAN STANDARD;
P15260;
O1-APR-1990 (Rel. 14, Created)
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                                                                                                                                            KTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKP
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                                                                                                                                                                                                                                                                 --LRVQASDGNNTSFWSEEI------KFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQ
                                                                                                                                                                                                                                                                                                    NGNIT-
                                                                                                                                                                                                                                                                                                                              YANMTFQVQWLHAFLKRNPGNHLYKW-KQIPDCENVKTTQCVFPQNVFQKGIYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                            NDPKSQTPSHPG-----WLMRG-----
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                                                                                                              KESLVISGLRHFTGYRIELQACNQDSPEERSGV-AAYVSARTMP
                                                                                                                                                                           TSSGNGAEDTRPSRKRRSLEEVGNVTATTPTLPDFPNISSTI--APTSHEEHRPFEKVVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 119; DB
Pred. No. 0.38
52; Mismatches
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POTENTIAL.
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IMPORTANT FOR BIOLOGICAL ACTIVITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
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                                                                                                                                                                                                        -TPVIQDYPLIYEIIFWENTSNAERKIIEK---
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4B919566902A944A CRC64;
                                    489
                                    8
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                                                                                                                                              431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                           804
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      TRANSMEM
DOMAIN
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   INTERFERON-GAMMA DIMER.

-!- SUBGULIT: MONOMER.
-!- SUBGULLUAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBGULLUAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PIM: PHOSPHORYLATED AT SER/THR RESIDUES.
-!- PIM: PHOSPHORYLATED AT SER/THR RESIDUES.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A., Wilkler F.K., Robinson J.A.;

"Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex.";

J. Mol. Biol. 273:882-897(1997),

-1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zauodhy P.J., Narula S.K.;
"Crystal structure of a complex between
soluble high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                            DOMAIN
                                                                                                                              CHAIN
                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                    EMBL; J03143; AAA52731.1;
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MEDLINE; 93183911
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Cell 55:273-280(1988).
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                                A LASSMANN H., Steck A.J.;

A LASSMANN H., Steck A.J.;

T "Expression and developmental regulation of Ehk-1, a neuronal TELK-like receptor tyrosine kinase in brain.";

L Neuroscience 63:163-178(1994).

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A2, -A3, -A4 AND -A5.

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A2, -A3, -A4 AND -A5.

C -!- FUNCTION: TYPOSINE PROSINE - ADP + APROTEIN TYROSINE - ADP + APROTEIN TYROSINE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

C -!- SINGELLULAR LOCATION: TYPE IN NEURONS.

C -!- SINGELLULAR LOCATION: TYPE IN NEURONS.

C -!- SINGELLULAR LOCATION: TYPE IN NEURONS.

C -!- STSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.

C -!- SINGLARITY: TO OTHER PROTEIN TYPE INILIZED DOMAINS.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)
KINASE RECEPTOR EHK.1) (EPH HOMOLOGY KINASE-1).
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                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 95206467.
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             This SWISS-PROT entry is copyright.
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PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE: PS01186; EGF_2; UNKNOWN_1.
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PFAM; PF01404; EPH_lbd; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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HSSP; P00523;
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                                                                                                                                                                                                                                                                                                                             470
                                                                                                                                                                                                                                                                                                                                                                   463
                                                                                                                                                        5.1%;
20.1%;
                                                                                                                                                                                                  111007
                                                                                                                                            51;
                                                                                                                                                                                                   ME:
                                                                                                                                                                                                          Score 118;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                          VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR RESDPPTMACTR -> G (IN SPLICED FORMS). RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
                                                                                                                                                                                                                                                                                                                                                                    GRRRTQGRGGG ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                  SGSCCECGCGRASSLCAVAHPSLIW ->
                                                                                                                                                                                                                                                                                             SPLICED FORMS
                                                                                                                                                                                                                                                                                                       TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA
                                                                                                                                                                                                                                                                                                                 KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMMADPLAHTNY
                                                                                                                                                                                                                                                                                                                                                         SPLICED FORMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPHRIN TYPE-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                             Mismatches
                                                                                                                                                                                                         ICED FORMS).

> E (IN REF. 2).

> A (IN REF. 2).

> A (IN REF. 2).

> A (IN REF. 2).

> I (IN REF. 2).

> I (IN REF. 2).
                                                                                                                                                                                                 1AED42C99693C574 CRC64;
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 ----CIKTTVENELPP------
                                                                                                                                                        DB
. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR 5
                                                                                                                                              165;
                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                   DADGPRAQASWCHARR (IN
                                                                                                                                                                   Length 1005;
                                                                                                                                              Indels 150;
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                                                                                                                                              Gaps
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 232
                    309
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                                     Query Match
Best Local Similarity
Matches 79; Conser
                                                                                                                                                                         TRANSMEM
DOMAIN
DISULFID
CARBOHYD
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Q61727;
                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstat. the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.; "A receptor for interleukin 10 is related to interferon receptors."; Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
-I- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6 X AJ F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL10RA OR IL10R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                             EMBL; L12120; AAA16156.1; -.
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                                                                                                                                                CARBOHYD
                                                                                                                                                              CARBOHYD
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13 LVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW----NRSDESVGNVTFSFDYQKT 68
                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PENIEVSVQNQNYVLKW------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFFKASPHSQTCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR---- 416
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                                                                                                                                                                                                                                                                     Transmembrane;
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263
204
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113
182
238
575
                                        Conservative
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                                                                                                                                                                                                                                                                                 IL10RA
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241
262
262
575
225
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238
                                    5.1s,
20.3s;
                                                                                                          64248 MW;
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                                                                                                                                                                                                                                                                    Glycoprotein; Signal
                                       47;
                                     Score 117.5; I
Pred. No. 0.15;
47; Mismatches
                                                                                                                                              POTENTIAL.
                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                         POTENTIAL. 820B9CD576F686B7 CRC64;
                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                         INTERLEUKIN-10 RECEPTOR.
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                                                     .15;
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                                                                DB 1;
                                        138;
                                        Indels 125;
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                                       Gaps
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RESULT 12
PTPD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pulldo R., Krueger N.X., Serra-Pages C., Saito H., Streuli M., "Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTPD_HUMAN
P23468;
                                                                                                                                                                                                                                                                            - i - (
                                                                                                                                                                                                                                                                                          MEDLINE; 91006018.

Krueger N.X., Streuli M., Saito H.;

"Structural diversity and evolution of human receptor-like protein
"Structural diversity";
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its the EMPL of the European Bioinformatics institutes and the EMPL outstation of the third through the substitution of the through the substitution of the through the substitutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphatase delta isoforms.";
J. Biol. Chem. 270:6722-6728(1995).
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Pulido R., Krueger N.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
TISSUES DUE TO ALTERNATIVE SPLICING.
PIM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
FROM THE TRANSMEMBRANE SEGMENT.
SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: PROTEIN TYROS: PROTEIN TYROSINE + ORTHOPHOSPHATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YIRHPG-----KLPTVLVFKKPHDFFPANPLCPETPDAIHIVDLEVFPKVSLELR
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                                                                                                                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE +
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         ormatics and the EMBL outstation
There are no restrictions on it
ong as its content is in no wa
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Query Match
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EMBL; X54133; CAA38068.1; -.
PIR; S12052; S12052.
HSSP; P18052; 1YFO.
MIM; 601598; -.
PRINTS; PR00014; FNTYPPITII.
PRINTS; PR007010; PRTYPHPHTASE.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
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                                                                                                                                                                                                                                                                                                   KNSEELYKEIDGVATTRYSVAGLSPYSDYEFRVVAVN----NIGRGPPSEPVLTQTSEQA 416
                                                                                                                                      ADSQITTIGNLVPQKTYSVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAEPESETS
                                                                                                                                                                          KTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSF 346
                                                                                                                                                                                                                  PSSAPRDVQARMLSSTTILVQWKEP-EEPNGQIQGYRVYYTMDPTQHVNNWMK----HNV
                                                         ILLSWTPPRS-----DTIANYELVYKDGEHGEEQRITIEPGTSYRLQGLKPNSLYYFR
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21.8%;
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PROTEIN-TYROSINE PHOSPHATASE.
PROTEIN-TYROSINE PHOSPHATASE.
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MISSING (IN KIDNEY ISOFORM).
MISSING (IN KIDNEY ISOFORM).
MISSING (IN FETAL BRAIN ISOFORM).
R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
MW; 3AEBCBCD32182E26 CRC64;
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CYTOPLASMIC (POTENTIAL).
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                               GCQNITSTKCNFSSLKLNVYEEIKL-----RIRAEKENTSSWYEVDSFTPFRKAQIG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by entities requires a licence are removed.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
M-PROTEIN, STRIATED MUSCLE.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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-!- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRIATED MUSCLE.
-!- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE
-!- PROPRIADMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AND CHARACTER AN
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21 LSAAAGGKNLKSPQKVEV-DIIDDNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLS
                                                                                                                                                                     Similarity
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IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

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IG-LIKE C2-TYPE DOMAIN.

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                                                                                                                                                                                                                Length 1450;
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Transferase

Glycoprotein;

/coprotein; Tyrosine-protein kinase; Phosphorylation; Transmembrane; Sign

Transmembrane; Signal;

ATP-binding nal; Repeat;

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EMBL; D37880; BAA07119.1; -.
HSSP; P11362; 1FG1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PFAM; PF00047; 19; 2.
PFAM; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P55146;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR
                                                                                                                                                                                                                                                                                                                                        Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
"Molecular cloning and in situ localization in the brain of rat sky
receptor tyrosine kinase.";
J. Blochem. 117:1267-1275(1995).
-!- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
IN THE CENTRAL NERWOUS SYSTEM.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
OTHER TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridaé; Murinae;
                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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SEQUENCE FROM N.A. STRAIN-BALB/C; TISSUE-BRAIN; MEDLINE; 96112625.
                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation u
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
                                   Eutheria;
                                             Eukaryota;
                                                     Mus musculus
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79; Conser
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Pred. No. 0.54; 
53; Mismatches 1
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IG-LIKE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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TYROSINE-PROTEIN KINASE RECEPTOR TYRO3
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                                            Craniata; Vertebrata;
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                                     Muridae; Murinae;
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EMBL; X85788; CAA59786.1; -. HSSP; P56276; ITLK.
MGD; MGI:94869; DCC.
PFAM; PF00041; fb3; 6.
PFAM; PF00047; fg; 4.
PRINTS; PR00014; FNTYPEIII.
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TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE
DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
BRAIN WITH VERY LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
BEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
AND REMAIN AT THIS LEVEL IN THE ADULT.
SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A FORM WHICH IS EXPRESSED ONLY: IN THE EMBRYO IS PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Transmembrane; Signal; Alternative initiation; Alternative splicing.
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
MISSING (IN EMBRYONIC ISOFORM).
MW; OD1F1097C2ZD5B9F CRC64;
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FIBRONECTIN TYPE-III.
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Query Match Best Local Similarity

4.8%; 21.4%;

Score 111.5; Pred. No. 1.

1.5; DB 1;

Length 1447;

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Search completed: June 1, 2000, 10:24:04 Job time: 20622 sec

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Best Local S
Matches 56
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PFAM; PF00041; fn3; 1.
PEQUENCE 349 AA; 39774 M
                   Q63953 PRELIN
Q63955;
Q1-NOV-1996 (Treme
Q1-NOV-1996 (Treme
Q1-NOV-1999 (Treme
Q1-NOV-1999 (Treme
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proteins.";
Gene 186:97-101(1997).
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Q61190;
Q61190;
Q1-NOV-1996 (TIEMBLIE). 01, Created)
Q1-NOV-1996 (TIEMBLIE). 01, Last sequence update)
Q1-NOV-1999 (TIEMBLIE). 12, Last annotation update)
CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 97199375. GIBBS V.C., PENNICA
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                           TTYCIQVQGFLLDQ -- NRTGEWSEPICERT -- GN 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSD 344
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                      6 (TrEMBLrel. 01, 06 (TrEMBLrel. 01, 19 (TrEMBLrel. 12, 19 (TREMBLREL. 12, 19 GAMMA RECEPTOR 2 (
                                                                                                                                                           PRELIMINARY;
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39774 MW; 4AC1802A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.6%; Score 222.5; DB 11
26.2%; Pred. No. 3.9e-10;
Live 47; Mismatches 82;
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(INTERFERON GAMMA RECEPTOR
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Matches 69
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REBOUL J., GARDINER N., "Comparative genomic analysis or receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1; -.
EMBL: AF082666; AAD13671.1; -.
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O9YGC8;
O1-MAY-1999 (TYEMBLIEL 1
O1-MAY-1999 (TYEMBLIEL 1
O1-MAY-1999 (TYEMBLIEL 1
INTERLEUKIN-10 RECEPTOR 2
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EMBL; U69594; AAC
EMBL; U69596; AAC
EMBL; U69597; AAC
EMBL; U69597; AAC
EMBL; U69598; AAC
EMBL; U69598; AAC
                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Entheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                     SEQUENCE FROM N.A.
REBOUL J., GARDINER K.,
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"A novel member of the interferon receptor family complements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94170381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
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AAB30165.
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                                                                                                                                           UZE G., LUTFALLA G.;
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GEISSEN M., HELLER S., PENNICA D., ERNSBERGER U., F
"The specification of sympathetic neurotransmitter
on gp130 cytokine, receptor signaling.";
Development 125:4791-4801(1998).

EMBL; AJ011688; CAB42084.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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GLYCOPROTEIN 130 PRECURSOR.
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VYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNH 273
                                                                                                                                                                                                                                                                                                          NIRYRISSDTNWMEVPP-EDTASPRTSFSIQGLRPYTEYVFSIRCMKEDGVGFWSDWSE-
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                                                                                   EPFEANGVILQYEVTIRAKPPLSHPPSRYNVTTTSLTLKLPNGTY----EVTVVAHNRVG
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Matches 106;
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Q9YHV9;
01-MAY-1999
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SEQUENCE
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
INTERFERON ALPHA/BETA RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative genomic analysis receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1; -. HSSP; P13726; ITFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LIVER;
REBOUL J., GA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHT 410
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           APKQSGNTPVI-
                                                                                                                                                                                                                                                                                                                              -- KAALLISWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEVFNSSLLH----FSPLSETFLGPPEFNLSSCVHCINITIKLPPTHLRKNGKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGT---KDSVMWALDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESVG---NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEE----IKLRIR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METLMGGPLRFYQLVFVSI----LCAACYSSLSEKIPREPPDNLQMTSNNFQHILSWRAHS
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                                                                                                                                                                                                                                                                                   LNKHSIPSAWK------CITTD------SVAEKDY---YGITIAGAICFSI
                                                                                                                                                                                                                                                                                                                                                                                           ---LSLFDIYNKVNYEITLRTVGEEHKRSPEKVTEEPFSIVIEELYPNRNYCVSVMVTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                              SFTYSLLIWKNSSGVEERIENIYSRHK------IYKLSPETTYCLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPTVPTYYRVLYS-----SHSNWKIAKQCSRIVQPFCNLTDDFQVVSDEYSAFVQSFVG
                                                                  KKK-----AEGSVGAVSSEDDSDDSESDAM-----
                                                                                                                FOKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYI-----G
                                                                                                                                                                      ILVVILKCLHL-----GGYILHKKSLPDTLVFTKMFSYLPFTFECEEITSVEIIY-KEV
                                                                                                                                                                                                                          -MTFQVQWLHAFLKRNPGNHLYKWKQIPD-----
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21.1%; Pred. No. (
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9; Mismatches 1
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Best Local Similarity 21.49
Conservative
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*Mouse Neogenin, a DCC-like molecule, has four sp.

expressed widely in the adult mouse and during em.

Oncogene 15:691-700(1997).

EMBL; Y09535; CAA70727.1; -.

EMBL; Y09535; CAA70727.1; -.

RSSP; P07251; ITTG.

MGD; MGI:1097159; Neo1.

RFAM; PF00041; Fn3; 6.

PFAM; PF00041; Fn3; 6.

PFAM; PF00041; FNTYPEIII.

REPAM; PF00041; FNTYPEIII.

REPAM; PF00041; FNTYPEIII.
  Q94537
Q94537;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TIEMBLIEL 03, Created)
01-MAY-1997 (TIEMBLIEL 03, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, 12, 14 annotation update)
NEOGENIN (NEOGENIN PROTEIN).
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                                                                                                                                                                     355 QSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 408
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                                                                                                                                                                                                                                                                                                                                                                                       TINGLKKYTEYSFRVVA--YNKHGPGVSTQDVAVRTLSDVPSAAPQNLSLEVRNSKSIVI
                                                                                                                                                                                                                                                   GIYLLRVQASDGNNT---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPK
                                                                                                                                                                                                                                                                                                                                        KW---DYTYAN---MTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APQSSDTSPVFVQHSTSSTCDGSSSWVSQNPDDGPEVFE---ENEMDAEE---EKDTDS
                                                                                                                               ENQNI-VVRGYAIGYGI---
                                                                                                                                                                                                                  TEYNFRVAALTVNGTGPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-VVSWTPP
                                                                                                                                                                                                                                                                                                  HWQPPSSTTQNGQITGYKIRYRKASRKSDVTETLVTGTQL-----SQLI--EGLDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                KIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVHLEAEDKAIVIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVENTSQPGEMQVTIQNLMPATVYIF-----KVMAQNKHGSG----ESSAPLRVET--QP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCQNITS-----TKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAPATTGPLPSAPRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTKEGVDR----E
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                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 130; DB 11; 21.4%; Pred. No. 0.063;
                                                                                                                             -GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75; Mismatches
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                      PRT;
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily and is required for Cell 87:197-204(1996).
EMBL; U71001; AAC47314.1; --
ELYBASE; FBGn0011592; fra.
FFAM; FF00041; fn3; 6.
PFAM; PF00047; 19; 3.
PFAM; PF000047; FNTYPEIII.
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01-FEB-1997
01-NOV-1999
                      1016
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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JAN L.Y., JAN Y.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                            TDVTVPNLKPLTVYCVKARAHT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A------NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLG
                    TMLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                         --HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVYSPVHCIKTTVENELP-----
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                                                                                                                                               LSDSFHIYIGAPKQSGNTPVIQDYP------LIYEIIFWENTSNAER-----KIIEKK 388
                                                                                                                                                                                                                                 DCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS
                                                                                                                                                                                                                                                                              APTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY----
                                                                                                                                                                                                                                                                                                                      WGRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVD
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                                                                                                         REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEE 1015
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AA; 151692 MW;
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02, Last sequence update)
12, Last annotation updat
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                      1037
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motor axon
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Best Local S
Matches 102
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JAN L.Y., JAN Y.N.;
"frazzled encodes a Drosophila member of the DCC imm
subfamily and is required for CNS and motor axon gui
Cell 87:197-204(1996)
EMBL; U71002; AAC47315.1;
FLYBASE; FB9n0011592; fra.
FFLYBASE; FB9n0011592; fra.
PFAM; PF00047; fn3; 6.
PFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
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Q94538;
Q1-FEB-1997
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Eukaryota; Metazoa; Arthropoda; Eracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQ 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGKNLKS-----PQKVEVDIIDDNFI-LRW-------NRSDESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                    WGRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVD
                                                                                                                                                                                                                           A-----NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLG
                                                                                                                                                                                                                                                                                    TGYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNR
                                                                                                                                                                                                                                                                                                            DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKI
                                                                                                                                                                                                                                                                                                                                         ISVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQI 837
                                                                                                                                                                                                                                                                                                                                                                     LSDSFHIYIGAPKQSGNTPVIQDYP------LIYEIIFWENTSNAER-----KIIEKK
                                                      ---HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSWSVLNSTYQNVPVTPP-----
                                                                                  DCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS
                                                                                                               APTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY----
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REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEE
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02, Last sequence up
12, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 129; DB 5; Length 1526; Pred. No. 0.078;
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"Neogenin, an avian cell surface protein expressed during terr RT neuronal differentiation, is closely related to the human tumc suppressor molecule deleted in colorectal cancer.";

RL J. Cell Biol. 127:2009-2020(1994).

DR EMBL; U07644; AAC59662.1; -.

DR HSSP; P80362; IWTL.

NR PFAM; PF00041; fig; 4.

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Q90610
RESULT
Q98949
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Best Local S
Matches 92
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O90610;
O1-NOV-1996 (TIEMBLIFEL 01, Created)
O1-NOV-1996 (TIEMBLIFEL 01, Last sequence update)
O1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
NEOGENIN (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
Q98949;
Q98949;
01-FEB-1997
01-FEB-1997
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MEDLINE; 95105243.
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                                                                                                                                                                                                                                                                                                                                                                                                           GCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                      LAPATTGPLPTAPRDVVATLVSTRFIRLTWRTPVSDPQGDNLTYSIFYTKEG----INRE 471
                                                                                                           ENQNI-VVRGYAIGYGI----GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                   OSGNTPVIODYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA
                                                                                                                                                              TEYNFRIAAMTVNGTGPATDWVSAETFESDLDESRVPEVPSSLHVRPLVTSI-VVSWTPP
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                                                                                                                                                                                                                                             ANMIFQVQWLHAFLKRNPGNHL----YKWKQIPDCENVKTTQCVFPQNVFQ--KGI---
                                                                                                                                                                                                                                                                       KYTEYSFRVVA--YNKHGPGVSTQDVVVRTLSDVPSAAPQNLTLEARNSKSIMLHWQPPP
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92; Conserv
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                                         PRELIMINARY;
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; Pred. No. 0.095;
61; Mismatches 2
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Last sequence update)
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RESULT
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Best Local Similarity
Matches 102; Conserv
                                                                                                                 092859;
Q92859;
01-FEB-1997 (TIEMBLIEL 0
01-FEB-1997 (TIEMBLIEL 0
01-NOV-1999 (TIEMBLIEL 1
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MEDLINE: 97067156.

BISCARDI J.S., DENHEZ F., BUEHLER G.F., CHESNUTT D.A., BARAGONA O'BRYAN J.P., DER C.J., FIORDALISI J.J., FULTS D.W., MANESS P.F. "Rek, a gene expressed in retina and brain, encodes a receptor tyrosine kinase of the Axl/Tyro3 family.";

J. Biol. Chem. 271:29049-29059(1996).
Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
[1]
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PFAM; PF00047; iq; 1.
PFAM; PF00069; PK1nase; 1.
SEQUENCE 873 AA; 96402 MW; 2918D55
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                         Homo sapiens (Human).
                                                                                                    NEOGENIN
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AXL-RELATED
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                                                                                                                       Created)
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Last annotation updat
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                                           Craniata; Vertebrata; Mammalia;
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                     Hominidae;
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                     Homo
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EMBL; U72391; AAC51287:1; -

HSSP; P02751; ITTG.

PFAM; PF00041; fn3; 6.

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EMBL; U61262; AAB17263.1; -.
HSSP; P02751; lTTG.
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PRINTS; PR00014; FNYYPEIII.
SEQUENCE 1461 AA; 159958 M
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MEDLINE; 97312699.
MEDLINE; 97312699.
VIELMETTER J., CHENG X.N., MISKEVICH F., LANE R.P., YAMAKAWA K.,
KORENBERG J.R., DREYER W.J.;
"MOLECULAR characterization of human neogenin, a DCC-related protein,
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurtheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity
Matches 93; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; F
                                                                                                                                                         "Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the nervous system of developing Xenopus embryos.";
Dev. Blol. 166:654-665(1994).
EMBL; U10986; AAA70168.1; -.
HSSP; P56276; lTLK.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1g; 4.
PRINTS; PRO0014; ENTYPEIII.
SEQUENCE 1427 AA; 156533 MW; E50B7475 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 95113183.
PIERCEALL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR SUPPRESSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEARON E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIILEHAP-----ATTGPLPSAPRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIYSRHKIYKLSPETTYCLKVKAALLISWKIGVYSPVHCIKTTVENELPPPENIEVSVQN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQIGPPEVHLEAEDKAIVIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGIARERVENTSHPGEMQVTIQNLMPATVYIF-----RVMAQNKHGSG----ESSAPLRV 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKSIMIHWQPPAPATQNGQITGYKIRYRKASRKSDVTETLVSGTQL-----SQLI--
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87; Conserv
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E 1461 AA; 160015 MW;
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Conservative
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Last annotation updat
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   Score 117.5; D
Pred. No. 0.59;
O; Mismatches
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                                                                    DB 13;
          163;
          Indels
                                                                    Length 1427;
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Xenopodinae;
          93;
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Query Match 5.1%; Score 117.5; D Best Local Similarity 19.7%; Pred. No. 0.68; Matches 86; Conservative 74; Mismatches
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Q17859; Q20137;
Q17859; Q20137;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z46811; CAA86842.1; -..
EMBL; Z49938; CAA86842.1; JOINED.
EMBL; Z49938; CAA90189.1; -.
EMBL; Z46811; CAA90189.1; JOINED.
HSSP; P28827; 1RPM.
PFAM; PF00041; fn3; 3
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RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEV-
                                                                                                 SFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEE 178
                                                                                                                                                          TFEVNVRRAYLFKVAAATMKGIGPYSPVLTINPDPADLILDNNIEEEEGNODPGEATMGE
                                                      NRNPPKKSKISTADVY-----SAILHHAPGP------LTHPISAALAKAKPTIGA
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1585 AA; 178386 MW; E403A8DD CRC32;
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396 LKPLTVYCVKARAHTM 411 't  :  :  :  :   635 LRPHMMYTIHVGVRTL 650	579 SVOLTMEYNG-PRNVGFYVNHTGRKDY-VNHELQEKTMSTPGFGQDVDEKHREYLWTN 634	526 VVSDLNAHKPYAFCVLAVKNIRQGPCSDPPTVL:: :   : :::   : ::   : ::   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : :   : : :   : : :   : : :   : : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : :   : : :   : : :   : : :   : : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :	291 CVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSD 344	471 ATSNSTAVVOMDFESQKADSFVVKYMHEPGNRMDTEKHKQLPVVSIDKENPKRFA 525	238 SVQNQNYVLKWDYTYANW-TFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTO 290	424 PMPAPYTTTSTPSTLFFQVTLPFMTTAWNRVTKLETLVGPPTNVRVE 470

Search completed: June 1, 2000, 05:54:18 Job time: 4523 sec

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A_Geneseq_36:W97861
A_Geneseq_36:R97469
A_Geneseq_36:R70149
A_Geneseq_36:R7013
A_Geneseq_36:R14641
A_Geneseq_36:R14641
A_Geneseq_36:R14641
A_Geneseq_36:W3147
A_Geneseq_36:W41803
A_Geneseq_36:R57139
A_Geneseq_36:R57139
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A_Geneseq_36:R571013
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A_Geneseq_36:W42087
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A_Geneseq_36:W52296
A_Geneseq_36:W75782
A_Geneseq_36:W79159
A_Geneseq_36:R71035
A_Geneseq_36:R75783
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Query: US-09-240-675-1
Query length: 1343
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Database sequences: 188963
Database length: 23686106
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A_Geneseq_36:R71723
A_Geneseq_36:W21805
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A_Geneseq_36:R42635
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A_Geneseq_36:R14488
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Sequence
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                 A_Geneseq_36:R85090
A_Geneseq_36:W09822
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-QB-A_Geneseq_36 -OPMT-fastan -SUFFIX-modif_rag -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOG-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOG-6.000 -DELEXT-7.000 -START-1 -MATRIX-bLosum52
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCt
-ALICN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                        A_Geneseq_36:R97
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IFN receptor extracellular doma
Spliced-deleted interferon alph
Spliced-deleted interferon alph
Spliced-deleted interferon alph
Spliced-deleted interferon alph
Spliced-deleted interferon alph
CRFB4 protein. New recombinant
IFN-gamma receptor beta-subunit
Zcytor7 cytokine receptor polyp
Human IFN-gamma accessory facto
IFN-gamma receptor beta-subunit
Human cytokine receptor 11 (Zcy
Human cytokine receptor 12 (Zcy
Plasmid pBABLUE human interfero
Extracellular domain of human in
Gamma-IFN-R-GBP 130 fusion prot
Gamma-IFN-R-GBP 130 fusion prot
Spliced interfero
                                                                                                                                                                                                                                                                   Gamma interferon receptor. New Gamma interferon receptor. New Rat receptor tyrosine kinase F Interleukin-10 receptor subunit! Mouse IL-10 receptor interleuk! Human LDL receptor analogue. I Gamma interferon receptor. New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble interferon-alpha/beta in Sequence of a soulble form of the Human alpha-interferon receptor Complete interferon-alpha/beta Sequence of a soulble form of the Human interferon receptor. Mond Human in receptor. Compsn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Documentation
                   Human Down syndrome-cell adhes Human Down syndrome-cell adhes Rabbit LDL receptor analogue. Extracellular domain of hybrid Rat REK7 eph-related tyrosine K EFF-like receptor protein tyros Human interleukin-12 receptor a
                                                                                                                                                             Soluble human interferon gamma Human neuronal calcium channe Human calcium channel alpha-2
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Deleted in Colorectal Carcinon
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A_Geneseq_36:W41804
A_Geneseq_36:W83927
A_Geneseq_36:R15049
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ID R14487 standard; Pr
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seq_name: A_Geneseq_36:R14487
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FR2657881-A.
09-AUG-1991.
05-FEB-1990; O01298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
Eid P, Gresser I, Lutfalla G
Tovey MG, UZe G;
WPI; 91-319778/44.
N-PSDB; Q14339
New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. claim 2; Page 45; 52pp; French.
The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.

Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble interferon-alpha/beta receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFN; autoimmune disease; graft rejection;
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Human IL-10 receptor. Int
Human T85 protein. New is
Hybrid human insulin-IGF-
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Quality: 2313.00 Ratio: 5.305 Percent Similarity: 100.000 x R14487 Length: 436 Gaps: 0 Percent Identity: 100.000

from: 1 to: 436

127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTC yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 126 34 17

AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 226 50

AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 276 67

84

**AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT** 376

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seq_documentation_block:
ID R28495
AC R28495
DT 31-MAR-1993 (first e
DE Sequence of a soulble
DE with a high affinity
Interferon receptor;
OS Synthetic.
PN W99218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; WO-F00318.
PF 17-APR-1991; WO-F0031
PA 1814 P, Gresser I, Lut
PI Tovey M, UZe G;
DR WPI; 92-382110/46.
DR N-PSDB; Q30532.
PT Water soluble polyper
and beta - useful as
PS Claim 2; Fig 1; 58pp;
CC DNA encoding the wate
CC IEN-alpha and -beta al
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US-09-240-675-1 x R28495
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Quality: 2313.00
Ratio: 5.305
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DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (30533), was incubated with oligos (30534 and 30535. R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind if IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.
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Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
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17-APR-1991; WO-F00318
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AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
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GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA
                               GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
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                     GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
                                                                roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
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alignment_scores:
Quality: 2313.00
Ratio: 5.305
Percent Similarity: 100.000
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US-09-240-675-1 x R11958
                                                                                                                                                           Align seg 1/1
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19-OCT-1990; F00758.
20-OCT-1989; FR-013770.
(CNRS ) CNRS CENT NAT RECH S
(CORS ) CNRS CENT NAT RECH S
MOGENSEN KE, UZE G, Lutfalla
WPI; 91-148740/20.
N-PSDB; 011701.
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                                                                                                                                                                                                                                                                                                      New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis
Disclosure; fig 4; 30pp; French.
This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residues 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
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Human alpha IFN; IFN agonists; antiviral; anti tumour drug targetting.
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                                                                     AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
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roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
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alignment\_block: US-09-240-675-1

x R14488 R14488

Align seg 1/1

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557

27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG

Quality: 2313.00 Ratio: 5.305 Percent Similarity: 100.000

Percent

Identity:

436 0 100.000

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alignment_scores:
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05-FEB-1990; O01298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
Eld P. Gresser I. Lutfalla G
Tovey MG, Uze G;
WPI; 91-319778/44.
N-PSDB; 014240.
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R14488 standard; Pr
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                                New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
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Complete interferon-alpha/Deta receptor.
IFN; autoimmune disease; graft rejection;
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458. .557
/label= cytoplasmic
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AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                            AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
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seq_documentation_block:
ID R28496; standard; Prot
AC R28496;
DT 31-MAR-1993 (first e
DE Sequence of a soulbie
DE MITT a high affinity
KW Interferon receptor;
OS Synthetic.
PN W09218626-A.
PD 29-OCT 1992.
PF 17-APR-1991; F00318.
PF 17-APR-1991; MO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-APR-1991; WO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-APR-1991; WO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-APR-1991; WO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-YBP; 92-382110/46.
DR N-PSDB; Q30533.
PT Water soluble polyper
PT and beta useful as
PT diseases and transple
PT and beta useful as
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PT and beta useful as
PT diseases and transple
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CC oligonucleotides as;
CC oligonucleotides as;
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CC treating autoimmune of
CC troic side-effects of
CC Sequence 557 AA;
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Tovey M, Uze G;

N wpr; 92-382110/46.

N-PSDB; Q30533.

N-PSDB; Q30533.

The soluble polypeptide(s) strongly bind interferon(s) alpha water soluble polypeptide(s) strongly bind interferon(s) alpha primater soluble polypeptide with a high affinity for diseases and transplant rejection claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for Claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the tis isolated by PCR, using appropriate coligonuclectides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30539), was incubated with oligos colors the transmembrane and cytoplasmic domains. Both forms bind complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind complete receptor with oligonal content of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of th
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alignment\_scores: Quality:

Ratio: Similarity:

2313.00 5.305 100.000

Length: Gaps: Percent Identity:

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06-0C7-1993;
31-MAR-1992; 400902.

31-MAR-1992; EP-400902.

(EUBI-) LAB EURO BIOTECHNOLOGIE S!
Benoit P, Maguire D, Meyer F, I
WPI; 93-312951/40.
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                          Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis

Disclosure; Fig 3, 21pp; English.

Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human if interferon alpha-beta receptor based on the second apparatus of the second apparatus of the second apparatus of the second apparatus of the second apparatus of the second apparatus of the second apparatus of the second are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment and second activities are useful for treatment activities are useful for treatment activities are useful for treatment activities are useful for treatment activities are useful for treatment activities are useful for the form activities are useful for the form a
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Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
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/label= extracellular_domain
/note= "soluble, immunogenic

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Quality: 2313.00
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23.MAR-1995.
16.SEP-1994; E03114.
17.SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE SA.
Benizri EJ, Tovey MG;
WPI: 95-131187/17.
N.PSDB; QB6458.
Compsn. of monoclonal antibodies against interferon recuseful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.
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Sequence 557 AA;
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                                                                                                                                   477 AAAGATAGTGTTATGTGGGCTTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                   377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         includes a 21-amino acid transmembrane region. Novel, splice-deleted IFWAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host-cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                   527
                                                                                                                                                                                                                                                                                                                                                     327
                                                      167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purposes.
Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804)
                                                                                                                                                                                                                                                                                                                                                                               - 84
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ATTCCAGACATAAAATTTATAAAACTCTCACCAGAGACTACTTATTGTCTA
                                                                                                                                                                                                                                                                                                         LysLeuArgileArgAlaCluLysCluAsnThrSerSerTrpTyrCluVa
                                               ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                  LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                           AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
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Ratio: 5.306
milarity: 99.771
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Gaps: 0
Percent Identity: 99.771
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3

IFN receptor extracellular domain.

IFN receptor; interferon receptor; interferon-alpha; interferon-beta; monoclonal antibody; immunomodulator; Homo; sapiens.

W09507716-A.

AIDS

R71723 standard; Protein; 436 AA.

16-OCT-1995 (first entry)

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seq_documentation_block:

ID R71723 standard; Prot
AC R71723;

DT 16-0CT-1995 (first e
DE IFN receptor extracel
KW IFN receptor; interfe
                                                                                                                         seq_name: A_Geneseq_36:R71723
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                                                                                                                                                                                                                                                                                                                                                  1227. GTATATTGTGAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA. 1276
                                                                                                                                                                                                                                                                                                                        401 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                              11772-TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 roProValPheAsnIleArgSerLeuSerAspSerPheH1sIleTyrIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   777 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 snileGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727 ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTÁT
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alignment_scores:
Quality: 2304.00
Ratio: 5.284
Percent Similarity: 100.000
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Benizri EJ, Tovey MG;
WPI; 95-131187/17.
N-PSDB; 086457.
Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS
Disclosure; Fig.2A-2B; 105pp; English.
Disclosure; Fig.2A-2B; 105pp; English.
A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coll or COS cell hosts: The protein was used to raise
                                                                                                                                            477
                                                 167
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Sequence 436 AA;
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                                                                                                                                                                                                                                                                                           MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                          AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTÄCÄTÄTÄGCTT 526°
                                                                                                                                                              ATTTAGAAGCTGAAGATAAĞGCAATAGTGATACACATCTCTCCTGGAACA 476
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                                             AspSerPheThrProPheArgLysAlaGlhfleGlyProProGluValH 134
                                                                                                                                                                                                                                                             TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
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                                                             ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT 576
                                                                                                   LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
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FE OS

w21805; 23-SEP-1997 (first entry) Spliced-deleted interferon Interferon alpha-receptor;

alpha-receptor form IFNAR.

Key

Location/Qualifiers
1. .427

Homo sapiens.

seq\_name: A\_Geneseq\_36;W21805

\_documentation\_block:

W21805 standard; Protein; 434 AA.

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1177
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                         1327 CCTCTAAA 1334
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hrSerLys
                                           ValTyrCysLeuLysAlaArgAlaH1sThrMetAspGluLysLeuAsnLy, 417.
                                                                                                        GTATATTGTGTGAAAGCCAGAGCACCACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                       TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                     TIGGTCTGAAGAGATAAAGTITGATACTGAAATACAAGCTTTCCTACTTC
                                                                                                                                                                                                                                                                                                                                                                          AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
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alignment_scores:
Quality: 2260.00
Ratio: 5.305
Percent Similarity: 99.766
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US-09-240-675-1 x W21805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: W21805 from: 1 to: 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNS alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also WZ1806) probably regulate
101
                                                                                                                                                                                              277 GTACCAMATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                           227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                               127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibiting, modulating or modi
Example 2; Fig 7; 46pp; Englis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian soluble interferon alpha-receptor forms
                                                                                                                                                                                                                                                                                                                                                                                      34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77. CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                    AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                          TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                          LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                         ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                     ANATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                      sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splice-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratovitski E, Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.766 Percent Identity: 99.766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ino acids 1-427 of the
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102 36 3 38 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	42 47 15
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	AACA Thr YThr GCTT
1184 676 676 676 676 676 677 676 677 677 67	476 150 526

Seq\_name: A\_Geneseq\_36:W21806

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alignment_scores:
Quality: 2208:00
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US-09-240-675-1 x-W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 3; Fig 7; 46pp; English.

C. (Wovel splice-deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also 773521) obtd. Crom human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNs, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or Sequence 496 AA;
                                                                                                                                                                                                                                                                                              Align seg 1/1 to: W21806 from: 11 to: 496
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                                                                                                                                                       127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
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24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LID.
(ABRA/) ABRAMOVICH C:
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Spliced-deleted interferon
                                    227
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                                                                                                                                                                                                   77 CCCATGGGTGTTGTCCGCÄGCCGCÄGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                            27 ATGATGGTCGTCCTGGGCGCGACGACCCTÄGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                              MetMetValValLeuLeuGlyAlaThrThrLeuValleuValAlaValGl 17
ntysvalGluvalAspileIleAspAspAspAspheileLeuAsgirpAsn
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Similarity:
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/label Extracellular_domain
/note "comprises amino acid
422-427 of transmembranal IFN
                                                                                                                                                                                                                                                                                                                                                                                5.282
97:892
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transmembranal IFNAR"
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Gaps: 1
Percent Identity: 97:892
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   GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA
                                              GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                    GGAATTTACCTTCTCCCCCGTACAAĞCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                          AAAATGTCAAAACTACCCAGTGTGTGTTTTCCTCAAAACGTTTTCCAAAAA
                                                                                                                                                                                                                                                 AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
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alignment_scores:
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                                                                                                                                                                                                                        US-09-240-675-1 x W52296
                                                                                                                                                                                                                                                                                   Percent Similarity: 60.268
  159 123 11 ... .. ... CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
KOTENKO SV, PESTKA S;
WPI; 98-110590/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rejection, as vaccine adjuvants, for treatment of photosensitivity, inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, viruses, bacteria and parasites (especially intracellular pathogens) and for preventing organ rejection: A vector containing (I) is used to restore, e.g. by gene therapy, II-10, sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit II-10 activity in cells. Antibodies specific for CRFB4 are used to measure and localise CRBF4, for diagnosis of defective II-10 activity. Fragments of (I) are used as primers or probes to assay CRFB4-specific RNA; Agonists/antagonists may be administered parenterally, orally or rectally especially by intravenous injection or directly into a tumour or allocated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the human CRFB4 sequence, DNA encoding it is used in the recombinant DNA (I) of the invention. (I) comprises a sequence (S1) encoding the interleukin-10 (II-10) receptor (III)R) and a sequence (S2) encoding CRFB4, both operably linked to expression control sequences. Cells containing (I) may be used to identify agonists/antagonist of II-10. Agonists are potentially useful, e.g. for preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRFB4 protein.
CRFB4; interle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 lelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                         81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laim 2; Page -; 79pp; English
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                                                          TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
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                                                                                                                                                                                                                                                                                                                               wality:
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                                                                                                                                                        to: W52296, from: 1
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                                                                                                                                                                                                                                                                                                 Percent Identity: 29.91
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                                                                                                            122
                118-00-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: A_Geneseq_36:R75782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh
W09516036-A.
15-JUN-1995.
07-DEC-1994; U14277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                                                                domain:
                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                            13-NOV-1995 (first entry)
IFN gamma receptor beta subunit.
Interferon-gamma receptor beta subunit; mulfN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
                                                                                                            domain
                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                    Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R75782 standard; Protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 ATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 TCATTCGATTATCAMAMACTGGGATGGATAMATTGGATAMATTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                      Interferon-gamma-antagonist:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 ThrAlaGlnTyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTACGTCATGGAMAATTGGTGTCTATAGTCCAGTACATTGTATMAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rThrHisAspGluThrValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGATACACATCTCCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elleGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet
                                                                             267. .33
/label=
                                                                                                                                                              243. . 266 .
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                       /label-
                                                                                                                                     label-
                                                                                                                                                                                                                                         label- Sig_peptide
                                                                                                            . 332
                                                                                                                                                              Extracelular domain
                                                                             Cytoplasmic_domain
                                                                                                                               Transmembrane_anchoring_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
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                                                                                                                                                                                                                                                                                                                       production of the second
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
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alignment_block:
US-09-240-675-1 x R75782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 203.00
Ratio: 1.471
Percent Similarity: 60.262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: R75782 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                           336 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig. 2A; 86pp; English.

The IFN-gamma receptor beta-subunit encoded by a CDNA clone derived
                                                                                              160
                                                                                                                                                                                                                                                                                                                  383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT
                                                                                                                                                                                                                                                                                                                                                                    110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be may be used to treat pathological conditions associated with endogenous may be used to treat pathological conditions associated with endogenous
171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL
                                           480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 ACAGGAGCGATGAGTCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFN-gamma production 
Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q90808
                                                                                                                                                                                                                                                                      126 oPheGlnH1sTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGUE/) AGUET M.
(BOEH/) BOEHNI R.
(HEMM/) HEMMI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr 32
                                                                                                                             GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                                alThrProGlyLysGlySerLeuValIleHisPheSerProProPheAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oLeuAsnProArgLeuH1sLeuTyrAsnAspGluGlnIleLeuThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC 124
                                                                                         .....ValPheHisGlyAlaThrPheGlnTyrLeuValHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boehn1 R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-164596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemm!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ......IleAspGlySerTrpHisArgLe 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 13
Percent Identity: 30.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s
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alignment\_block: US-09-240-675-1 x W79159

Percent Similarity: 50.346

Gaps: 17
Percent Identity: 21.016

Length:

Can

Quality: 198.00

Align seg 1/1 to: W79159 from: 1

8

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18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 57 CIAGIGCICGICGCCGIGGGCCCAIGG.....GIGITGICCGCAGCCGC

34

alignment\_scores:

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seq_name: A_Geneseq_36:W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                  binding receptor polypeptide and is a novel member of the type 2 cytokin receptor. family (CRF2). An expression vector containing the Zcytor polynucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transform host cells for the recombinant production of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
Sequence
                                                                preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor? can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO.) ZYMOGENETICS INC.
Adams RL, Farrah TM, Jelmberg AC, Kho CJ, Lok S,
Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zcytor7 cytokine receptor polypeptide.
zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor; family; CRF2; prostate tissue; nervous tissue; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 .GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624 CTAMAAGTTAMAGCAGCACTA...CTTACGTCATGGAAAATT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
                                        also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                               Claim 1; Pages 55-59; 72pp; English.
This represents the Zeytor7 cytokine receptor. Zeytor7 is a ligand-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 CCAGACATAAAATTTAT.....AAACTCTCACCAGAGACTACTTATTGT
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; V5751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W79159 standard; Protein; 553 AA.
                                                                                                                                                                                                                                                                                                                                                                   Novel human Zcytor7
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 98-480798/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1998; U03029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO9837193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural disease;
                                                                                                                                                                                                                                                                                                                                                for treating renal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1998 (first entry)
  553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "intracellular domain"
                                                                                                                                                                                                                                                                                                                                            DNA encodes a type
neural, pancreatic
                                                                                                                                                                                                                                                                                                                                            2 cytokine receptor - useful and prostatic diseases
                                                                                          proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662
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25 pProLeuSerGlnLeuProAl	The state of the s	923 HAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACAT 972
108AAAAATCTAAAATC		
60 GTGCTCGTCGCCGTGGGCCCA :::   :::\  :::    9 LeuLeuLeuLeuClyVal		281 ysGluLysHisProAlaAsnLeuIle
Align seg 1/1 to: R71035 fr		САТТТСТАТАЛАТССАЛАСЛАЛТАССТСАС
alignment_block: US-09-240-675-1 x R71035		776 TACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCCAGGCCTTTT 822
Quality: 155.50 Ratio: 1.030 Percent Similarity: 50.333		726 AATARAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTA 775    ::::::::     259    IleSerIleThTVal
SO Sequence 337 AA; alignment scores:		245 erGluPheLysAlaLysIleIlePheTrpTyrValLeUPro
PS Disclosure Fig 21A; 114p CC The sequence is that of h CC Incorporation of AF-1 int CC normal function with elim		gAlaGlnProSerGluLysGlnCys
DR N-PSDB; 084697. PT Suppressing tumours in ma PT for interferon gamma, spe PT antigens, including use o		ola ACIACITATIGICITAAAGITAAAGCAGCACTACTACGTATGGAAAAT 661            ::::    :::::::::::::::::::
(UYNE-) UNIV Cook JR, Dor Pestka S, Sch WPI; 95-10667		
PN W0950847-A. PD 02-MAR-1995. PF 22-AUG-1994; U09438. PR 20-MIG-1993; US-110119		518 ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG 567
DT 11-OCT-1995 (first entry DE Human IFN-gamma accessory KW Interferon-gamma; AF-1; t		480GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517
seq_documentation_block: ID R71035 standard; Protein; AC R71035		445 AGGCAATAGTGATACACATCTCTCCTGGAACAAAA
		395 TCGCANAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA 444
ATTTTTTGGGAAAACA        :::::   epheCysaspSerG	P	345 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGAGTCATTTACACCATT 394 :::    :::          -         -     -     -     -      -      -       -       -
		298 CACTCAAGCTGAATGTTTATGAAGAATTTAAATTGCGTATAAGAGCA 344 :::::::::::::::::::::::::::::::::::
		248 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297 ::::
	· · ·	198 AATGTGACTTTTCATTCATTATCAAAAAAACTGGGATGATTATTGGAT 247 :::     :::::::   :::::::::::::::::::
		151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG 197 :: ::: :::   ::: :::     49 snMetLysAsnValleuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
	· · · · · · · · · · · · · · · · · · ·	101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150            :::      ::::: 34 rGlyGlyLeuProLysProAlaAsnIleThrPheLeuSerIleA 49
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Align seg 1/1 to: R71035 from: 1 to: 337

SCCC SP P P P P P P P P P P P P P P P P	R P P P P P P P P P P P P P P P P P P P	seq		
Suppress; No Suppress; No Suppress; For Interactions antigens, Disclosur The seque Incorpora normal fur Sequence	documentation_block: R71035 standard; Pr R71035; 11-OCT-1995 (first Human IN-gamma acc Interferon-gamma; A Homo sapiens W09505847-A HOMO-1994; U09438 22-AUG-1994; U09438 22-AUG-1999; U09438 22-AUG-1998; US-110 (UYNE) UNIV NEW JE Cook JR, Donnely R Pestka S, Schwartz WPI; 95-106679/14 N-PSDR: OAA667	1140 369 1190 385 name:		297 973 310 1014
Suppressing tum for interferon antigens, inclu Disclosure, Fig The sequence is Incorporation o normal function Sequence 337	ocumentation_bloc R71035 standard; R71035; R71035; R71035; I1-OCT-1995 (fir Human IR- gamma a Interferon-gamma; Homo sapiens. Homo sapiens. Homo sapiens. Homo sapiens. Homo sapiens. Homo sapiens. Ugyara. Homo sapiens. Ugyara. Homo sapiens. Ugyara. Homo sapiens. Ugyara.	ATTTTTGGG	CCATA:	
sing tumours sing tumours erferon gamm is, including us, Fig 21A pence is tha ration of AF function wit ie 337 AA;	standard; p ; ; 1995 (firs IFN-gamma ac eron-gamma; apiens apiens 1995, 1994; U0943 1994; U0943 1993; US-11 1995, 1993; US-11 1994; US-11 1995; US-11	rreco	rCTAT;	rgPhel rgGTC: :: IleTh: CCTAC: - - -
ours gamma ding 21A that that f AF witl	# E # E	ATTITITGGAAAACACTTCAAATGCTGAGAAAAATTATCGAGAAAAA	CCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGCCCTGTGATCC	
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n mammals w specifical se of AF-1 i 114pp; Engl of human ini into immunu elimination	337 ) fact umouz anuel h J;	CAAATGCT ::   ::: !!uAsnThr GTTCCTAA :::    TleProPr	CAAAAC   ::: roGlnF GAAATT ::::::	AAAGTTI  :::  :::  CTTTAL
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		ATGTTCTTAAATGGGATTATATATGCAAACATGACCTTTCAAGT	757
		4.	259
	756	CAAAATCAG	744
•	259	ThrGluLeuGlnGlnValIleLeuIleSerValGlyThrPheSerLeuLe	243
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•	242		226
-	710	TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATG	561
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	622	TCCAGACATAAAATTTA	579
	192		178
	5 7 8 20	TTATCTGGAAAACTCTTCAGGTGTAGAAAAG	Š
	178	S eAlaAspThrSerThrAlaPhePheCysTyrTyrValH	165
	7 'i		70
	165	:::    :::    : ThrProGlyGluGlySerLeuIleI	49
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•	387 133	<pre>l AGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTA                    galaGluLeuGlyAlaLeuHisSerAlaTrpValThrMetProTrpPheG</pre>	141
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	340	CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAG	ĕ
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	299	AGAATATTACTAGTACCAAATGCAACTTTTCTTCA	265
	87	TrpPheTh;AlaAs	74
	264	GATGGATAATTGGATAAAATTGTCT	33
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	58		42
	182	1 ATGACAACTTTATCCTGAGGTGGAACAGGAGC	151

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Database: Issued_Patents_AA:*
Database sequences: 145308
Database length: 14437401
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Query length: 1343
Database: Issued_Patents_
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-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-LOOPEXT-0.000 -QGAPEXT-4.500 -QGAPEXT-0.550 -XGAPOP-10.000
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-MATRIX-blosum62 -TRANS-human40.cdi -LIST-45 -DOCALIGN-200
-THK_SCORE-pct -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3
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                                                                                                                                                                                                              Align seg 1/1 to: US-08-307-588-2 from: 1
                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                                     27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGG
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                    77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
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Ratio: 5.305
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US-08-307-588-2
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-537A-103+
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-424-788-2+ 117
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-110-683-4+ 117
                                                                                                                                                 TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acids
TOPOLÓGY: linear
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release $1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/ACENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MONOCLONAL TITLE OF INVENTION: RECEPTOR, V
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3000 K St
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGUIRE, Deborah
PLAVEC, Ivan
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Length: 436
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227

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377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
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                                                   TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                     GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                         GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10
                                                                                   TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1227
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                                                                                                                                                            REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
MOLECULE
                                                                                                                                                                                                                              APPLICATION NUMBER: IL 107
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 hrSerLys. 436
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                                                                                                                         TELEPHONE: 202-737-3528
                              STRANDEDNESS: single
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                                                                  ENGTH:
                                             i: 557 amino acids amino acid
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                        APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                         MEDIUM TYPE: Floppy
               FILING DATE: 24-OCT-
                                                                   "SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
                                                                                    OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                  CITY: Washington
                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08328256
                                                                                                                                                                                                                                                     419 Seventh Street,
                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   BROWDY AND NEIMARK
9 Seventh Street, N.W.,
                                                                                                                                         Floppy disk
                                   24-OCT-1994
IL 107378
                                                 US/08/328,256
                                                                                      Release #1.0;
                                                                                      Version #1.30
                                                                                                                                                                                                                                                       Suite 300
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US-08-328-256-10

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alignment_block:
US-09-240-675-1 x US-08-328-256-10
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Ratio: 5.305
Percent Similarity: 100.000
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                                                                                                                                                                                477. AAAGATAGTGTTATGTGGGCTTTTGGATGGTTTAAGCTTTACATATAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                    LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                  ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
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                                        ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT
                                                                                                                                                        AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
OPERATING SYSTEM: PC

disk

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seq_documentation_block:
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                                                                                                                                                                                                                                                                   Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL, INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UTFALLA, Georges
APPLICANT: LUTFFALLA, Georges
APPLICANT: GRESSER, ION
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1227
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ADDRESSEE, NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON TARGINIA TURGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1327 CCTCTAAA 1334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
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alignment_block:
US-09-240-675-1 x US-08-471-454-2
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                                                                                                117
                                                                                                                                                                                   101 LysLeuArglleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
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134 isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
                                            427 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                           277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                        227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77. CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 yProTrpValLeuSerAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 816-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BYRNE, THOMAS E. REGISTRATION NUMBER: 32,205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                        lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
                                                                                                                      TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                  AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                              erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                            sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
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1327 CCTCTAAA 1334         434 hrSerLys 436	1227 GTATATTGTGTGAAAĞCCAĞAĞÇACAĞAĞGATGAATAA 1276	1127 GATTTATGAAATTÄTTTTTTGGGAÄÄAAACACTTCAAATGCTGAGAGÄÄÄAAA 1176	27 CTCCAGTCTTÄACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 10	877 AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAAA 926	727 ATATAGAAĞTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776	27 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 67	477 AAAGANAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT 526

seq\_name: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:US-08-466-974-2

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alignment_scores:
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127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
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APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
                                                                                                77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2
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                                                                                                         NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 01.0,
CURRENT APPLICATION DATA:
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 96 PELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDMBER OF SEQUENCES: 2
ORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C
                                                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: UFILING DATE: 15-JUN-1
          STRANDEDNESS:
                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/471,453 FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA 1276
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200797 NIXN UR
                                   amino acid
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LUTFALLA, Georges
GRESSER, Ion
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APPLICANT: TOVEY MICHAEL G. T. ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
TOTAL OF INVENTION: INTERFERON
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APPLICANT MEYER, Francois
APPLICANT MAGUIRE, Deborah
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7277 GTACCAAATGCAACTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
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                                                         427 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AAATTGCGTÄTAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                              117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH
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ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
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REFERENCE/DOCKET NUMBER:
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1127 GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
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                                                                         1327 CCTCTAAA 1334
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                                                                                                                                                                                                                                                                                                                                                                                                     1177: TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT: 1226:
                                                                                                                                                                                                                                                                                                                                             367. ulleTyrGlulleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677 AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
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434 hrSerLys 436
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                                                                                                                                                           AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                                                   GTATATTGTGTGAAAGCCAGAGCACCACCATGGATGAAAAGCTGAATAA 1276
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                                                                                                                               sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT
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alignment_block:
US-09-240-675-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11near, molecule TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
OPERATING SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: REVEL, Michel
APPLICANT: ABRANOVICH, Carolina
APPLICANT: ARAPOUTSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERPERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 24-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                     127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                   34
                                                                                                                        77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                             27 ATGATGGTCGTCCTGCGCGCGCGACGACCTAGTGCTCGTCGTCGTGGG
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, ROGER L
REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                   lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                  yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                            MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Gaps: 0
Identity: 100.000
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ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy

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1077
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351 GlyAlaProLysGlnSerGlyAsnThrProVallleGlnAspTyrProLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
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                                                                                                                     CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
                                                                                                                                                                                                                                                                      GlylleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
                                                                                                                                                                                                                                                                                                         GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976
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                                                        GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                               eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP. 334
                                                                                                                                                                                                                TIGGICIGAAGAGAIAAAGIIIGAAACIGAAAIACAAGCIIICCIACIIC 1026
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                                                                                                  roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
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alignment_scores: 0.00 Quality: 2213.00
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STATE: D.C.
COUNTRY USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION DATA:
APPLICATION MUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION MUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY ROGER L.
                                                                                                                                               , MOLECULE TYPE: protein US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            TELEPHONE: 202-628-5197
TELEPRA: 24863
TELEX: 24863
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1227 GTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1277 AAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1177 TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1127 GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: REVEL, Michel APPLICANT: ABRAMOVICH, Carolina APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 TelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 sSerSerValPheSerAspAlaValCysGlu 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 ulleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401: ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, ROGER L.
REGISTRATION NUMBER:, REVEL-13
REFERENCE/DOCKET NUMBER: 25,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Application US/08328256 5643749
  Ratio: 5.282
larity: 98.126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EE: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
  Percent Identity: 98.126
                       Length:
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Align seg 1/1

to: US-08-328-256-12

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US-09-240-675-1 x US-08-328-256-12

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127 AAAAAGTAGAAGGTCGACATACATAGATGACAACTTTATCCTGAGGTGGAAC 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
251 ThrTyrAlaAsnMetThrPheGlhValGlnTrpLeuHisAlaPheLeuLy 267
                                                                                                                                                                                                                                                                                                        234 snileGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 LysvallyshlahlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                             ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTGGGATGGATAAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                   oValHisCysIleLysThrThrValGluAsnGluLeuProProProGluA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isLeuGluAlaGluAspLysAla[leValIleHis]leSerProGlyThr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
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                                                        AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                        sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                    AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG '876
                                                                                                                                                                                                                                                                                                                                                                               ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANAGTTANAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1177
                                                     TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1077. GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 194004
COMPUTER READABLE FORM:
MEDIUM TYPE: 5,25 inch., 360 Kb floppy, disk
COMPUTER: IBM FC compatible
COMPUTER: TOWN PMS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1277 AAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                     REFERENCE DOCKET NUMBER: 86
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415/25-5530
TELEPAX: 415/952-9881
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SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acid
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ...08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT, APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bohn1, Ruth
APPLICANT: Hemm1, Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
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                                                                                                                                                                                                              FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 460 Point San Bruno Blvd
CITY: South San Brancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aguet, Michel
                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1994
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                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-4
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US94-14277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1 x PCT-US94-14277-3
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                                                     Sequence 4, Application:
                                                                                                                                                                                                                             201 AsnLys 202
                                                                                                                                                                                                                                                                                                                                                                                         655 GGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAA 704
                                                                                                                                                                                                                                                                                                                                          184 ysLysHisSerAsnTyrSerThr***G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 LysLysThrIleAsnSerThrTyrTyrValGluLysIleProGluLeuLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555 GAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 ysProSerPheSerTyrThrIleArgIleTrpGlnLysSerSerSerAsp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505 GTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 GATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 HisMetSerProProGluValArgLeuGluArgGluAspLysAlaIleLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 CAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 GAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAAC. 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 GGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GluCysGlnHisThrThrThrThrLysC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 erThrSerSerTrpAsnGluValAspProPheIleProPheTyrThrAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCAGAGACTACTTATTGTCTAAAAAGTTAAAGCAGCACTACTTACGTCAT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                 uProGluThrThrTyrCysLeuGlu***LysAlaIleHisproSeftLeuL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uValHisIleSerProProGlyGlnAspGlyAsnMetTrpAlaLeuGluL 134
                                                                                                                                                                                                                                                                               AATGAA 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT 404
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                                                                                  Application PC/TUS9414277
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Aguet, Michel
Bohni, Ruth
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3.337
72.772
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Percent Identity: 48.515
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-1 x PCT-US94-14277-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                        858 AAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCC 907
                                                                                                                                                                                                       808 GGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAAACCATTTGTATAAATGG 857
                                       908 TCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTG 957
                                                                                                                                                                                                                                                                                                                                                                              711 CTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGT 760
                                                                                 51 LysProIleProThrCysAlaAsnValGlnThrThrHisCysValPheSe 67
                                                                                                                                                                                                                                                                                          761 TCTTAAATGGGATTAT...ÀCATATGCAAACATGACCTTTCAAGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
67 rGlnAspThr***TyrThrGlyThrPhePheLeuHisValGlnAlaSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                      1 MetProValProGlyAsnLeuGlnValAspAlaGlnGlyLysSerTyrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Love, Richard B. REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/164596
                                                                                                                                                                  rpLeuProGlyTyrSerLysSerSerSerGlySerHisSerAspLysTrp 50
                                                                                                                                                                                                                                                   lLeuLysTrpAspTyrIleAlaSerAlaAspValLeuPheArgAlaGlnT
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73.558
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84
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1008 ATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGA 1057

84 luGlyAsnHisThrSerPheTrpSerGluGluLysPheIleAspSerGln

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958 ATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAA 100

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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-683-743-4
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-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensach Ave, Continental Plaza,
STREET: Floor
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                                                                                           HYPOTHETICAL:
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                                                                                                                                         OLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      LENGTH:
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TLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TLE OF INVENTION: CHAIN
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                                        TYPE:
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                                                                                                                                                                                                                                                                                                                       325 amino acids
                                                                                                                                                                        linear .
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                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABLUSTED STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALL TO BE STORY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4th
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seq\_documentation\_block:

Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
CAPPLICANT: Aguet, Michel

seq\_name: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:PCT-US94-14277-2

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alignment_block:
US-09-240-675-1 x US-08-683-743-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 228.50
Ratio: 1.693
Percent_Similarity: 60.268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-683-743-4 from: 1
212 rThrHisAspGluThrValPro 219
                                                                                                                                                       645 CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC
                                                        695 CACAGTTGAAAATGAACTACCT 716
                                                                                                             196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh 212
                                                                                                                                                                                                                  179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu
                                                                                                                                                                                                                                                                       595 ATARACTOTORCOAGAGACTACTTATTGTCTARAAGTTARAGCAGCAGCACTA 644
                                                                                                                                                                                                                                                                                                                               162 YThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                                                                               545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                       146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 GATGGTTTA....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 TGATACACATCTCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 ACTICITCAIGGIAIGAGGIIGACICATIIACACCATIICGCAAAGCICA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 TTATCCTGAGGTGGAACAGGAGCGAATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 ThrAlaGlnTyr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 snileLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eIleGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 29.911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325
                                                                                                                                                                  694
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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: PCT-US94-14277-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5:25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                         207 TTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                          254 G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                              175 ACAGGAGCGATGAGTCT...
                                                                                                                                                                                                                                                                                                                                                                               125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 86
FELECOMMUNICATION INFORMATION: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg 109
                                                                                                                                                                                                                                                                                                                                   32 oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 TIGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG 93
                                                                                                                                                                      66 TyrSerPhe...
                                                                                                                                                                                                                                                                                                                                                                                                                         16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/CFILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/10 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
                                                                                                                                                                                                                                                     luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.262
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Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 30.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         866PCT
                                                                                                                                                                    .IleAspGlySerTrpHisArgLe 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from:
                                                                                                                                                                                                                                                                                              .....GTCGGGAATGTGACT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 332
                                                                                                                                                                                                                                                                                                                                        49
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seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-2
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                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6627
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/80
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ent No.
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 alThrProGlyLysGlySerLeuValIleHisPheSerProProPheAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624 CTAAAAGTTAAAGCAGCACTA...CTTACGTCATGGAAAATT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 CCAGACATAAAATTTAT....AAACTCTCACCAGAGACTACTTATTGT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 oPheGlnHisTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 382
                                                               REGISTRATION NUMBER: 32,743
                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1201 E
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Jelmberg, Anna C. : Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Lox, Si
: Kho, Choon J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Farrah, Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ication US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZymoGenetics, Inc
                                                                                                  Paul G
                                                                                                                                                    UMBER: 08/803,305
20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...ValPheHisGlyAlaThrPheGlnTyrLeuValHi 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theodore E
                                                                                                                                                                                                                                                                               US/08/943,087
                                                  96-24C1
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; TOPOLOGY: 1in
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-2
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US-09-240-675-1 x US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 50.346 Percent Identity: 21.016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 eLeuGluThrGlnIleGlyProProGluValAlaLeuThrThrAspGluL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150
                                                                                                                                                 568 AAAATATTTATTCCAGACATAAAATTTATAAA.....CTCTCACCAGAG 611
                                                                                                                                                                                                    182 nValSerValLeuAsnThrLysSerAsnArgThrTrpSerGlnCysValT 199
                                                                                                                                                                                                                                                       166 GluAspLeuProValSerMetGlnGlnIleTyrSerAsnLeuLysTyrAs 182
                                                                                                                                                                                                                                                                                                                                                             480 .....GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517
                                                                                                                                                                                                                                                                                                                                                                                                           149.ysSerIleSerValValLeuThrAlaProGluLysTrpLysArgAsnPro 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 AGGCAATAGTGATACACATCTCCTGGAACAAAA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC 100
212 ThrLeuTyrCysValHisValGluSerPheValProGlyProProArgAr 228
                                                   612 ACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAT 661
                                                                                              34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 553 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 198.00
Ratio: 0.908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 553
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17
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ž	TREET: 12	DDRESSE	NUMBER OF SEQ	CANT:	••••	LICANT:	documentation quence 14, App tent No. 59455	seq_name: /cgn2_6/	385 nGluSerLeu	**		342	4	327 MetSerLeu		973 CTTTTGGT	923 AAAAGGAATTT :    :::: 297 pLysArgPheP	0	873 TGTGAAAAT		264 eLeuphese	•	259IleSerI	. 5-	erGluP	711	::: 228 gAlaGlnPro	662 Testercia
	I Eastlake Av le	ZymoGenetics, Inc.	. H	Theresa M.	obyn L.	ION: k, S1 o, Choon J.		/ptodata/1/1aa/5B_COMB.	SerArg	AAAACA ::::: spSerG	:::  ngluGluGluGluValLysHisLeuGlyTyrAlaSerHisLeuMetGlu	АСТБАТТТА	CCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTG	GCTTTCCTRCTTCTCCASTCTTTAWCATTAWATCCCTTAWSTORTTCATT	snPheIleThrLeuAsnIleSerAspAspSerLys	TGGTCTGAAGAGATAAAGTTTGATAC:	TACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACAT :::::: ;PheValproAlaGluLysIleValIleA	Le	TGTGAAAATGTCAAAACTACCCAGTGTGTCT?	SHisProAlaAsnLeuIle	eLeupheSerValMetGlyTyrSerIleTyrArgTyrIleHisValGlyL TaaaaaGGaaTCCTGGaaaCCATTTGTATTABATGGAAACAaATGACTTGAC	TACATATGCAAACATGACCTTTCAAGTT(	IleThrVal	AGT	 heLysAlaLysIleIlePheTrpTyrValLeuPr		;;; gAlaGlnProSerGluLysGlnCysAlaArgThrLeuLysAspG	TGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA
	<u>.</u>		TOX					pep:US-08-943-087-14	ThrileProProAspLysThrVallleGluTyr 4		rAlaSerHisLeuMetGlu	ArgProPro	GGAAACACGCCTGTGATCC		rLysileSerHisGlnAsp	TGAAATACAA		eTyrGlyAsnGluPheAs	TTCCTCAAAACGTTTTCCA		_	CTCCACGCCTTTT:::		ATGTTCTTAAATGGGATTA	 rValLeuPro	CTACCTCCACCAGAA	::::: lnSerS	•
				:-		· •		· - :	101	) : w ` <del>   </del>	6	352 1139	, ,	341	326	1013	972 310	297	922	289	281 872	822	264	775	258	725	245	710

STATE: WA COUNTRY: USA ZIP: 98102

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                       395 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA 444
                                                                                                                                                       345 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 394
                                                                                                                                                                                                                                                       298 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 344
                                                                                                     116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150
                                                                                                                                                                                                                                                                                                                                                               248 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                          99 laGluThrSerAspTyrGluHisGluTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                               82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                               66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORMATION FOR SEQ ID NO: EQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/803,305 FILING DATE: 20-FEB-1997 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/943,087 FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECOMMUNICATION INFORMATION ELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 21.016
from: 1 to: 553
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9									
	385 p	1114 A 352 1 1140 A 369 1	1014 G 327 M 1064 C 342	923 A 297 p 973 C 310 s	823 T 281 Y 873 T 290 .	726 AA 259 776 TA 264 eL	228 g 711 ·	568 A 199 h 612 A 212 T	445 A 149 Y 166 G 518 A
, cyne_0/ p	nGluSerLeuS	GATTATCC	ETTTCCTAC             stSerLeuL   CATATCTAT	AAAAGGAATTTACCTTCT       :::::::::::::::::::::::::::	AAAAAGGAA :::::::::::::::::::::::::::::	ATATAGAAG	GGLGTCTAT	AAAATATTTA     hrasn ACTACTTATT     	AGGCAATAGTU    :::    ysSerIleSe ysSerIleSe
רטממרמ/ ד/	SerArgThrI	AGGATTATCCACTGATTTATGAAATT	TTCCTCCAG	TACCTTCTC ::::: PheVal TGAAGAGAT ::::  TLeuAsnIl	TCCTGGAAA:   :::   sProAlaAs TCAAAACTA	ATAGAAGTCAGTGTCC	AGTCCAGTA	TTCCAGACA	SATACACAT  STATE
/ - 3 - 4 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5		1114 AGGATTATCCACTGATTTATGAAATT	1014 GCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATT	923 AAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACAT 972 :    297 pLysArgPhePheVal	TAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGAC ::::::::::   :::   ysGluLysHisProAlaAsnLeuIle TGTGAAAATGTCAAAACTACCCAGTGTGTGTTTCCTCAAAACGTTTTCCA :::::::   :::	AATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTA    ::::::	TGGTGTCTATAGTCCAGTACAGTGTATAAAGACCACAGTTGAAAATGAA. ::::	AAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAG	AGGCAATAGTGATACACATCTCTCCTGGAACAAAA      : : :
. рер . ос	11GAMACCA     AspLysThr	GlyTyralase TGAGAGAAAA :   :   rGluGlyThrs	TTAGATCCC ::	GTACAAGCATCTGATGGAAATAACACATProAlaGluLyslleVallleA GTTTGATACTGAAATACAA	TTTGTATAAATGGAAACAAATACCTGAC ::: ulle	ACTATGTTCCAGTGG	AAGACCACA :::    ArgThrLeu C7	TAAA LLeuThrTI CACTACTTA ::: heValProc	AACAAAA
00 040	ValileGlu	THISLEUM	TTAGTGAT	GGAAATAA LysileVa 'A eSerHisG	AAAACGTT	TTAAATGG	ACAGTTGAAAATGAA. :::::::: LeuLysAspGInSerS .CTACCTCCACCAGAA .	CTCTCACCAGAG	pLysArgAs GTTTAAGC: ::   :: :snLeuLys :snLeuLys :::::
	111 111 11yr 401	etGlu 368	341 341 3ATCC 1111 3Prog 352	ACACAT 972 alileA 310CAA 101 ;;; alnasp 326	TIGAC 872 289 22 111: 297 297 297 297 297 297 297 297 297 297	GGATTA 775Ph 264 CCTTTT 822 alGlyL 281	rgaa. 710 :::: 245 nsers 245 DAGAA 725	CCAGAG 611    :::  ProAsn 211  GAAAAT 661  :::  OArgar 228	3nPro 165 FTTAC 517 ::::: Tyras 182 3ATTG 567 :::: 3ValT 199

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alignment_block:
US-09-240-675-1 x US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-16
                                                                                                                                                                                                                          Align seg 1/1 to: US-08-943-087-16 from: 1 to: 553
                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 197
                                                                                                            101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                            57 CTAGTGCTCGTCGCCGTGGGCCCATGG......GTGTTGTCCGCAGCCGC 100
49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: WA
COUNTRY: USA
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREET: 1201 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997
                                                                                                                                               LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECOMMUNICATION INFORMATION: ELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
                                                                       rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553 amino acids
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Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farrah, Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZymoGenetics, Imc.
01 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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internal
                                                                                                                                                                                                                                                                                                                 198.00
0.908
50.346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theodore E.
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                                                                                                                                                                                                                                                                                                                   Percent Identity: 21.016
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1063	GCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATT	1014
326	snPheIleThrLeuAsnIleSerAspAspSerLysIleSerHisGlnAsp	310
1013	CTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAA	973
310		297
972	TCCGCGTACAAGCATCTGATGGAAATAACACAT	923
297		290
922	TGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCA	873
289	ysGluLysHisProAlaAsnLeuIle	281
872	GAAACAAATACCTGAC	823
281	eLeuPheSerValMetGlyTyrSerIleTyrArgTyrIleHisValGlyL	264
822		776
264		259
775	erdupnetysalatysilellephetrptyrvalteupro	7 .4.5
725	CTACCTCCAGAA	711
245.	gAlaGlnProSerGluLysGlnCysAlaArgThrLeuLysAspGlnSerS.	228
710	TGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA.	662
228	:::    ::::: ::: ::: ThrLeuTyrCysValHisValGluSerCheValProGlyProProArgAr	212
661	ACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAT	612
211		199
611.	AAAATATTTATTCCAGACATAAAAATTTATAAA	UT 10
199		182
567	ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG	518
182		166
517	.>-	480
165	wsserIleSerValValLeuThrAlaProGluLysTrpLysArgAsnPro	149
470		A
149	TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA :::::::::::::::::::::::::::::::	395 132
132		116
394	GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTTACACCATT :::    :::	345
115	<b>o</b> .	99
344	CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA	298
99		. 82
297	-	248
82	LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe	66
247	-	198

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	luTyr 401	385 nGluSerLeuSerArgThrIleProProAspLysThrValIleGluTyr 401	385
	TATAT 1232	1190 AACTGATGTTACAGTTCCTAATTTGAAACCACTGACTGTATAT 1232	1190
	urGlnGl 385	369 IlePheCysAspSerGluGluAsnThrGluGlyThrSerPheThrGlnGl 385	369
	GAAAAA 1189	1140 ATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAA 1189	1140
	MetGlu 368	352 inGluGluGluGluValLysHisLeuGlyTyrAlaSerHisLeuMetGlu 368	352
	1139	1114 AGGATTATCCACTGATTTATGAAATT	1114
	roProG 352	342ProGlnProSerGlyAsnLeuArgProProG 352	342
٠.	FGATCC 1113	1064 CCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCC 1113	1064
	3p 341	327 MetSerLeuGlyLysSerSerAspValSerSerLeuAspAsp 341	327

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Search information block:
Query: US-09-240-675-1
Query length: 1343
Database: PIR_63:*
Database sequences: 168808
Database length: 58629743
Search time (sec): 70.990000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pir2:A56178
pir2:T16040
pir2:A44027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: Jun 1, 2000 5:46 PM
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-O'-/cgn2_1/USPTO_spool/US09240675/runat_30052000_165118_2984/app_query.fasta.1
-O'-/cgn2_1/USPTO_spool/US09240675/runat_30052000_165118_2984/app_query.fasta.1
-DB-PIR_63 -OPMT-fastan -SUFFIX-modif.rpr -GAPOP-12.000
-GAPEXT-4.000 -MWANTCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.500
-OGAPOXT-4.000 -OGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOXT-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCt
-ALIGN-15 -MODE-LOCAL -OUTENT-Pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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US-09-240-675-1 x A32694
Align seg 1/1 to: A32694 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 ATGATOGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
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Ratio: 5.305
Percent Similarity: 100.000 Per
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F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
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Length: 436 Gaps: 0 Percent Identity: 100.000

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1177
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                                                                                                                                                                                                                                                                                                                                                                                            301 GlyIleTyrLeuLeuArgValGinAlaSerAspGlyAsnAsnThrSerPh
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1227 GTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA 1276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
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                                                                       TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT
                                                                                                         ulleTyrGlulleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI
                                                                                                                                               GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                   GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
                                                                                                                                                                                                                   GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                                      roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                                                                                                                                                                                                                         CTCCAGTCTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC
                                                                                                                                                                                                                                                                                                                      eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                             TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC
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interferon alpha receptor type 1 precursor - bovine C; Species: Bos.primigenius taurus (cattle) (c; Date: 13-Jan-1995 #text_change 05-Nov-1999 C; Date: 13-Jan-1995 #text_change 05-Nov-1999 C; Accession: S27387; S33770 C; Accession: S27387; S33770 R; Mouchel-Vielh, E; Lutfälla, G.; Mogensen, K.E.; Uze, G. FEBS lett. 313; 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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A;Experimental source: lung

C;Reywords: antiviral; cytokine receptor; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha interferon
A;Reference number: S33770; MUID:93305725
A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Specific antiviral activities of the human alpha interferons are determine A;Reference number: S27387; MUID:93076908
A;Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1 x S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molécule type: mRNA
A;Residues: 1-421, 'Y',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571:1; PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Eim, J.K.; Langer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1507.00 Length: 439
Gaps: 64.920
Percent Similarity: 86:105 Percent Identity: 64.920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align Seg 1/1 to: $27387 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: EMBE:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
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                                                 230 TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
65 uGlyThrAspAsnTrpLysLysLeuSerGlyCysGlnHisileThrSerT
                                                                                                                                                                                                                                                                                                           16 grrpValleuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA 32
                                                                                                                                                                                                                                                                                                                                               80 ATGGGTGTTGTCCGCAGCCGGAGGTGGAAAAAATCTAAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 ATGGTCGTCCTCGTGGCCGCGACGACCCTAGTGCTCGTCGCCCGTGGGCCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGATGAGTCTGTCGGGÁATGTGACTTTTTCATTCGATTATCAAAAAAC 229
                                                                                                                           SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGlnIleLe
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1168 AGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAA 1217
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                                                                                                                                                                                                                                                                                 1021 TACTTCCTCCAGTCTTTAACATTAGĀTCCCTTĀGT...GĀTTCATTCCAT
                                                                                                                                                                                                                                                                                                                                                                                     971 ATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                299 SerArgGlyIleTyrTyrYalArgValArgAlaSerAsnGlyAsnGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 hrvalTyrProGluAspLysIleTyrLysLeuSerProGluIleThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 ATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTAT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          921 CAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 snCysGluAsnValThrSerThrHisCysValPheProArgGluValSer 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ePheLysLysIleProGlyAsnHisSerAspLysTrpLysGlnIleProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                771 GATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTT 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721 CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 TAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 GGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 AMATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 CCAAATGCAACTTTTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                    TTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspTyrProTyrGluAsnAlaThrPheGlnAlaGlnTrpLeuArgAlaPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAATTGGTGTCTA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyThrLysAspSerIleMetTrpAlaMetAspArgSerSerPheArgTy 165
                                                                                                                                               ValSerValGlyAlaSerGluGluSerGluAsnMetSerValAsnGlnLe 365
                                                                                                                                                                                                                                                   lePheProProValIleSerValLysSerValThrAspAspSerLeuHis
                                                                                                                                                                                                                                                                                                                                                        rSerPheTrpSerGluGluLysGluPheAsnThrGluMetLysThrIleI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roGluAsnIleGlnIleAsnAlaAspAsnGlnIleTyrValLeuLysTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rSerProValTyrCysIleAsnThrThrGluArgHisLysValProSerP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysLeuLysValLysAlaGluLeuArgLeuGlnSerArgValGlyCysTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alHisLeuGluAlaGluAspLys&laIleIleLeuSerIleSerProPro 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uValGluProPheValProPheLeuGluAlaGlnIleGlyProProAspV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLeuArgIleArgAlaGluGluGlyAsnAsnThrSerThrTrpTyrGl 115
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A; Molecule-type: DNA
A; Residues: 426-445 <RE65
A; Cess-references: EMBL:006242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A; Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A45283; I48423; I48424; I48425; I48426; R; Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
                                                                                       A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:A45283
Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
                                     ; Residues: 473-590 < RE7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Mus musculus (house mouse)

Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999;

Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999;

Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999;
                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                         Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ne 148, 343-346, 1994
Title: Structure of the murine interferon alpha/beta receptor-encoding gene: Reference number: I48423; MUID:95047447
Accession: I48423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.
Note: sequence extracted from NCBI backbone Aurory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reference number: A45283; MUID:92262522
Accession: A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Picss-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary, translated from GB/EMBL/DDBJ 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lolecule type: DNA
lesidues: 265-375 <RE4>
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Residues: 118-125 <RES>
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                                                                                                                                                                                                                                                                                                  ss-references EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
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                                                                                                                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 177/3; 331/1 C;Keywords: cytokine receptor;

transmembrane protein

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alignment_scores:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                 167 eArgIleTrpGlnLysSerSerSerAspLysLysThrIleAsnSerThrT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 TGGGATGGATAATTGGATAAAATTGTCTGGGTGTÇAGAATATTACTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GlnAspGlyAsnMetTrpAlaLeuGluLysProSerPheSerTyrThrIl 167
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                                                                                                                                                                                                                                627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTTGGTGTCTATAGTCC 676
                                                                                                                                                                                                                                                                                                                                      577 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
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                                                                                                                                              677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 hrLysCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 sAspGluAlaLysTrpLeuLysValProGluCysGlnHisThrThrThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArgThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 snileAspValTyrileIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                             727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                          ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGATÄGTGTTÄTGTGGGCTTTGGÄTGGTTTÄAGCTTTACÄTATAGCTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgLeuGluAlaGluAspLysAlaIleLeuValHisIleSerProProGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluValLysAlaileHisProSerLeuLysLysHisSerAsnTyrSerTh 217
                                                                                                                                                                                                                                                                                yrTyrValGluLysIleProGluLeuLeuProGluThrThrTyrCysLeu 200
snLeuGlnValAspAlaGlnGlyLysSerTyrValLeuLysTrpAspTyr
                                        ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776
                                                                                           rValGlnCysIleSerThrThrValAlaAsnLysMetProValProGlyA 234
                                                                                                                                       AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
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Ratio: 3.230
milarity: 75.917
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Percent Identity: 48.624
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submitted to the EMBL Data Library, April 1994
A; Reference number: G06935
A; Accession: G01418
A; Status: preliminary; translated from GB/EMBL/
                                                                                                                                                                                                                                                                                                                     cytokine receptor family II, member 4 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
A;Gene: GDB:CRFB4; CRF2-4
A;Cross*references: GDB:1381.68; OMIM:123889
A;Map postition: 21422.7-21422.7
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                         A;Cross-references: IMBL:U08988; NID:9571295; PID:9571296
C;Genetics:
                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:G01418
                                                                                                                                                                                                                                                                            Accession: G01418 -- Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1224 ACTGTATATTGTGTGAAAAGCCAGAGCACACCATGGATGAAAAAGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1274 TAAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924 AAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               874 GTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           824. AAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 IleAlaSerAlaAspValLeuPheArgAlaGlnTrpLeuProGlyTyrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ... ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rLysSerSerSerGlySerHisSerAspLysTrpLysProIleProThrC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nLysThrSerAsnPheSerGluLysLeuCysGluLysThrArgProGlyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yLeuAsnTyrGluIleIlePheTrpGluAsnThrSerAsnThrLysIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAA 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAsnCysGlnAspSerThrCysAsp...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrGlyThrPhePheLeuHisValGlnAlaSerGluGlyAsnHisThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erMetGluLysAspGlyProGluPheThrLeuLysAsnLeuGlnProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCC 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrValTyrCysValGlnAlaArgVal...LeuPheArgAlaLeuLeuAs
                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           member 4 -
                                                                                                                                                                                                                                                                                                                          #text_change 17-Jul-1998
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cytokine receptor family class II protein CRF2-4 precursor - human
                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                               eq_name:
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                                                                     Species: Homo sapiens (man)
Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-240-675-1 x G01418
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Percent Similarity: 61.161
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                           Accession: A
Lutfalla, G.
                                                                                                                                                                                                                                                                                  '212 rThrHisAspGluThrValPro 219
                                                                                                                                                                                                                                                                                                                                                                                               196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh
                                                                                                                                                                                                                                                                                                                                     695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 TACAC...ATCTCTCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 ACTICTICATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 GATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 ThralaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 snileLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eIleGlyProProGlyMetGlnValGluValLeuAspAspSerLeuHisM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                   pir2:A47003
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366-373, 1993
                                                         A47003
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Percent Identity: 29.911
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alignment_block:
US-09-240-675-1 x A47003 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A47003; MUID: 93300510 A; Accession: A47003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: A47003 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-325 <LUT>
Cross references: GB:Z17227; NID:g393378; PID:g393379
196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh 212
                                                    645 CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC
                                                                                                     179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu
                                                                                                                                                            595 ATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA: 644
                                                                                                                                                                                                              162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                      146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                     501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 TGATACACATCTCTCCTGGAACAAAAGATAGTGTT. . . ATGTGGGCTTTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG 453
                                                                                                                                                                                                                                                                  545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                         129 etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 eileGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357; ACTICTICATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 HisSerAspTrpValAsnile...ThrPheCysProValAspAspThril 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 snileLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 29.911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tokine receptor gene family maps on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
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alignment_scores:
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A;Title: CRF2-4:isolation of cDNA clones encoding the human and mouse proteins. A;Reference number: JC6311
A;Recession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: p1r2:JC6311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA
;Residues: 1-349 <GIB>
;Cross-references: GB:U53696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterferon receptor-class II cytokine receptor mouse

Species: Mus musculus (house mouse)

Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 rThrHisAspGluThrValPro 219
                                                                                                                                                                                                                                                                                                                                                                                               363 TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 GAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 GGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 TCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 CAA....AAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 265
                                                                        492 TGGGCTTTGGATGGTTTA.....AGCTTTACATATAGCTTACTTATCTG 535
                                                                                                                                131
                                                                                                                                                                                                                                        114 yProProGluMetGlnIleGluSerLeuAlaGluSerLeuGluLeuArgP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                             463 TCTCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 rpGluValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                                          99 GluTrpValAsnVal...ThrPheCysProValGluAspThrIleIleGl 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGlnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAGAAATTAAATTGCGTATAAGAGCAGAA: . . AAAGAAAACACTTCT 362
                                                                                                                                                                                                                                                                                          TCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                       yrGlyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sArgThrAlaSerThrGlnCysAspPheSer.....HisLeuSerLysT 82
TrpThrLeuLysAsnIleTyrAspSerTrpAlaTyrArgValGlnTyrTr 159
                                                                                                                              heSerAlaProGlnIleGluAsnGluProGluThr
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1.582
61.404
                                                                                                                                                                                ......CCTGGAACAAAAGATAGTGTTATG 491
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Percent Identity: 28.070
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382 109

uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG

.93

297 76

93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg

254 G. ... TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT

TyrSerPhe...

207 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 253 49 luproSerProSerSerAsnAspProArgProValValTyrGlnValGlu

.....IleAspGlySerTrpHisArgLe

175 ACAGGAGCGATGAGTCT.....

....GTCGGGAATGTGACT 206

65

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R; Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M. Cell 76, 803-810, 1994.
Cell 76, a novel member of the interferon receptor family complements functionality A; Reference number: A49947; MUID:94170381
A; Accession: A49947
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                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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C; Species: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-332 <HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interferon gamma
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                                                                                                                                                                                                                                  US-09-240-675-1 x A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; Species: Mus musculus (house mouse)
Date: 06.0ct-1994 #sequence revision 1
                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross references: GB:S69336; NID:g545841; PIDN:AAB30165.1; PID:g545842; Experimental source: early B-cell line Y16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 pLysAsnGlyThrAsnGluLysPheGlnValValSerProTyrAspSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 ATARAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             686 TATAAAGACCACAGTTGAAAATGAACTACCTCCA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 GlyPheLeuLeuAspGlnAsnArgThrGlyGluTrpSerGluProIleCy 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      636 GCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 luValLeuArgAsnLeuGluProTrpThrThrTyrCysIleGlnValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 s...GluArgThrGlyAsnAspGluIleThrPro
                                                      125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                   87 TTGTCCGCAGCCGCAGGTGGA.....AAAAATCTAAAATCTCC
32 oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
                                                                                                16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine receptor
                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-332 <HEMD
                                                                                                                                                                                                                                                                                                                             Ratio:
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                                                                                                                                                                                                                                                                                                   203.00
1.471
60.262
                                                                                                                                                                                            from: 1
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13
30.131
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us-09-240-675-1 x I38500
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                                                                                                                                                                        Align seg 1/1 to: 138500 from: 1 to: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           esidues: 1-63,'Q',65-337 <RE2>
ross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olecule type: mRNA sesidues: 1-63,'Q',65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 CCAGACATAAAATTTAT.....AAACTCTCACCAGAGACTACTTATTGT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 oPheGlnHisTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GIGCICGICGCCGIGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 alThrProGlyLysGlySerLeuVallleH1sPheSerProProPheAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT 429
                                                         9 LeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaProProAs 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma receptor accessory factor-1 precursor - human
... AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source: clone pSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                            50.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of an accessory factor required for activation of MUID:94170380
                                                                                                                                                                                                                                                                                                                         Percent Identity: 22.33:
      150
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276 eu	259 757	744	711	226	209	579 193	529 178	165	435 149	388 133	341 116	300 104	. 265 . 87	233	183	151	25
euIl	uSer ATGT	Thre			TCTA      sLeu										· .		
eLysTy	ValLe.	luLeut	CTCCAC	TGTCT/   YH1SL	TCTAAAAGTTAAAGCAGCACTACCTTACGTCA.	GACAT	CTGGA    : rTrpG	AGATAGTGTTATGTGGGCTTTG :::::    ::: eAlaAspThrSerThrAlaPhe	roGly	ATTTC :::  sTyrA	GAAAA     GluLe	hePro	AGAATATTACTAGTACCAAATGCAACTTTTCTTCA :::      ::::   :::    ::::   hrGlnIleThrAlaThrGluCysAspPheThrAlaAlaSer	GATGGATAATTGGATAAAATTGTCT	AGTCT	CAACT	LeuSe
TTTP	ATGGG	GlnGlnValIle	CAGA	ATAGTO	AAAGC	AAAATT Serile	AAAACT :: Lu	TATGTO	GAAGA:	GCAAA     ::: rgasn	AGAAA uGlya	CTCAA	CTAGE   ::: hrAla	TTGGA:	GTCGG	TTATC	rGlnL
heH1s	YALAC ATTAT	Walil	AATAT	CAGTA	AGCAC	TAT	CTTCAG :::  LysG	GGCT1	TAAGGG	SCTCAC	ACACT LaLeuI	GCTGAJ :::  pPheas	ACCAA.	TAAAA: :: heThr/	GAATG: :::  rargv	CTGAG	euProi
ThrPr	ysPhe ACATA	eLeuI	AGAAG	CATTG     SerCy	TACTT	uAspa	GGTGT	TGGAT	AATAG	ATTGG :::   ValG1	TCI      1sser	TGTTT        nVal.	ATGCAL 	TGTĆI	rGACTT	STGG.	AlaPro
oProS	PheLei	leSer	TCAGT	TATAA     :	ACGTC	AACTC ::    snLeu	AGAAG ; yIleG	GGTTT	TGATA	TCCTC	TCATG :::   AlaTr	ATGAA	CTTTI :   :	Пеме	TTTCA   :::	uProv	SlnHi
erIlei	IVALLA ACATG	ValG1	STC.	AGACCI	A nLysSerA	TCACC	AAAGG ::::: lnGln	AAGCT	CACAT	CAGAA        roGlu	GTATG	GAAAT	CTTCA :::::	tSerI	TTCGA	alala	sProL
roLeu	uLys1	ThrP		ACAGT1	erAsn	AGAGA(  :::  SerA	ATTGA: ::::: Vally:	TTACA	CTCTC	GTACA	AGGTT	TAAAT   ThrL	Alase	 1eGlyv	TTATC:	LeuSe	ysIle
eullelystyrTrpPheHsThrProProSerTleProLeuGln[1eGlu	USETVALLEUALAGIYALACYSPhePheLeuValLeuLySTYFATGGIYL	alGlyThrPheSerLeuLeCAAAATCAGAACT		TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA	TCTAAAAGTTAAAAGCAGCACTACTTACGTCATGGAAAA      :::   :::    :	TCCAGACATAAAATTTATAAACTCTCACCAGAGAGCTACTTATTG	TTATCTGGAAAAACTCTTCAGGTGTAGAAAGGAAAGGATTGAAAATATTTAT         : : : : : : : : : : : : : : : :	AGATAGTGTTATGTGGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTAC	GCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAA :::	CACCATTTCGCAAAGCTCAGAATGGTCCTCCAGAAGTACATTTAGAA :::   ::::::    1nHisTyrArgAsnValThrValGlyProProGluAsnIleGluVal	AGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTA	CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAG :::       GlyPheProMetAspPheAsnValthrLeuArgLeuAr	AGAATATTACTAGTACCAAATGCAACTTTCTTCA	GATGGATAATTGGATAAAATTGTCTGGGTGTC         :::       	GATGAGTCTGTCGGGAATGTGACTTTTTCATTCATTATCAAAAAACTGG	ATGACAACTTTATCCTGAGGTGGAACAGGAGC:::::::::::::::::::::::	pProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA
		euLe			AAAA Argv	PATTG	TTTAT		ACAAA AspIl	NA	ATTTA     pPheG	ATAAG :::   LeuAr	erAla	GGGTGTC :::   alasnCysT	ACTGG	GGAGC ::: erThr	uTyrA
292	276 806	259 756	743	710	660 226	622	578 192	528 178	478 165	434	387 133	340 116	299 103	264 87	232 73	182	42

\_name: pir2:T13822

	alProPheAsnArgAsnGlyMetGlyAspSerSerAlaGluIleArgVal 646	.630
	CACCATTTCGCAAAGCTCAGATTGGT413	388
	uAlaValLeuThrGluLeuArgProHisThrAspTyrvalIleSerValV 630	. 613
	GTTGACTCATTTA 387	375
	SerGluAsnAspSerGlyAlaAspLeuTyrHisAspSerThrAlaLeuGl 613	597
	374	374
	   lugluproThrValThrAsnGlÿGlüfleLeuLÿšTyrArğVálTyřTÿr~596	580
	ATGAG	370
	AFRAGAGCAGAAAAAGAAACACTCTTCATGGT 369	563
	ThrGinProGluValAsnTleAlaGlyProProAr	
	AGAATATTACTACTACCAAATGCAACTTTTCTTCA. 299	٠ .
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•	ıProLeuGlnAsnAlaGlyAspValValTyrTyrThrValTyr	
:	TCAMARASTANASTONASTANASTANAS TITALE CLIMBS 1/1	463 172
	g 1/1 to: T13822 from: 1 to: 1375	Align seg
	_block: 0-675-1 x T13822	alignment_block: US-09-240-675-1
	C. SCORES: C. SCORES: C. Constity: 129.00 Ratio: 0.542 Ratio: 0.542 Similarity: 38.264 Percent Identity: 16.399	Percent Similar
receptor mediating N	A; Description: may function in vivo as a receptor or component of a	A; Descrip
		A; Gene: fr A; Map posi C; Function
AC47314.1	type: mRNA 1-1375 <kol> erences: EMBL:U71001; NID:gl</kol>	A; Molecule A; Residues: A; Cross-ref
	number: 217780 T13822 eliminary; trans	ess:
subfamily a	7-204, 1966 7-204, 1966 azzled encodes a Drosophila member of the DCC immu	Cell 87, 197-2 A;Title: Frazz
S.; Jan, L.Y.; Jan,	<b>&gt;</b> ,	0

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910	883 834 899	849 777 866	776 833 776	799 771 816	738 785 770	717	663 744 713 751	581 710 631 727	680 531 696	414 647 434 663 683
ATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGA :::	AAAAGGAAT::::    .sinlysAsnGlnHisvalThrAspAsnArgHisTyrThrValSerTyrGl	ThrProLeuGluValProValGlyLeuArgAlaI GACCTTCAAGTCAGTGGCTCCACGCCTTTTTA .::::: !   rSerIleValValTyrTTpileAspThrMetLeu		pGluAsnThrIleGluLeuLysGluThrGluArgTyrHisIleLeuLysA ( GATTAT GATTAT (	AGTGTCCAAAATCAGAACTATGTTCTTAAATGG		GGTGTCTATAGTCCAGTACATTGTATAAAGACCACÁGTTGAAAATGAACT	CAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAG ::::::::::::   ::::::   ::::   :::   :::		# # GT - B
929	833 899 879 910	824	776 849 776	816 776 832	770 799 770	737	712 751 716 768	630 727 662 743	695 580 710	433 663 480 530

R;Vielmetter, J.; Kayyem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A;Title: Neogenin, an avian cell surface protein expressed during terminal neuronal A;Reference number: A55193; MUID:95105243

C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 13-Sep-1996

A;Cross-references: EMBL:U07644; NID:g641965; PID:g641966

Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-1443 <VIE>

alignment\_scores:

Quality: Ratio: Percent Similarity:

127.50 0.644 47.711

Length: 415
Gaps: 19
Percent Identity: 22.169

alignment\_block:

US-09-240-675-1 x I50600 Align seg 1/1 to: I50600

87 TTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGA 136

from: 1 to: 1443.

seq\_documentation\_block:
neogenin - chicken (fragment)

5.3 5.4 3.4 6.4 seq\_name: pir2:150600

A CONTRACTOR OF STREET	A:CLOSS TETERENCES: GB:M39014, NID:9204953; PIDN:AAA41441.1; PID:9204954 C:Superfamily: Insulin receptor; protein kinase homology C:Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; F:1032-1398/Domain: protein kinase homology CKIN> F:1030-1038/Region: protein kinase homology CKIN> F:1030-1038/Region: protein kinase homology CKIN>	ion: A36080  preliminary  le type: mRNA  es: 1-1383 <601>	R:Goldstein, B.J:, Dudley, A.L. Mol. Endocrinol: 4, 235-244, 1990 A:Tille: The rat insulin receptor: primary structure and conservation of A:Reference number: A36080; MUID:90231337	or - Fat 0.00 to 500 to 1. icus (Norway rat) uencerevision 14-Dec-1990 atext change 18-	seq_name: pir2:A36080 seq_documentation_block:	1206 CCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCA 1250	1159 CARATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTT 1205	1109 GATCCAGGATTATCCACTGATTTATGAAATTATTTTTTTT	1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGT 1108	1018 TCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGAT 1058 :::	972TCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTT 1017	933TACCTTCTCCCCCGTACAAGCATCTGATGGAAATAACACA971	898 GTGTCTTCCTCAAAAGGTTTTCCAAAAAGGAATT	849 .TATABATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGT 897	813 CACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTG	763 TTANATGGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTC 812	716 TCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTC 762	
	4954 in; transmembrane p		n of tissue-specifi	Jun-1999														
782 TGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGA 831	GTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATA	691 AGACCACAGITGAAAÄÄGAACTACCTCCACCAGAAAATATAGAAGTCAGT 740	G00 eSeraspGluargargThrTyrGlyalaLysSeraspIleIleTyrValG 617	600 CTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTAC 649	550 GTGTAGAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAA 599 583 583				( i 🖚	300 CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAA 349 550 550		oAspPheArgAspLeuLe	AAAACTGGGATGGATAAT :::   ::::   ::: ArgThrSerPheAspLysIleLe	ACAGGACGATGAGTCTGTCGGGAATGTGACTTT	125 TCAAAAAGTAGAGGTCGACATCATAGATGACCAACTTTATCCTGAGGTGGA 174         :::::            ::::::	1-675-1 x A36080	0.645 41.561 Percen	127.00

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C;Accession: A31555
R;Aguet, M:; Dembic, Z:; Merlin,
Cell 55, 273-280, 1988
                                                                                                                                                                              A;Title: Molecular cloning and expression of the human interferon-gamma receptor. A;Reference number: A31555; MUID:89003065 A;Accession: A31555:
                                                                                                                                                                                                                                                                                                                interferon gamma receptor precursor - human
C; Species: Homo sapiens (man)
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                        A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1:489, <AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                eq_name: pir2:A31555
                                                                                                                A;Cross-references: GB:J03143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1159 CAAATGCTGAGAGAAAAATTATCGAGAAA......AAAACTGATGTT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1300 TATGTGAGAAAACAAAACCA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1250 ACACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTG 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669 LeuPheGluLeuAspTyrCysLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 AATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655 .........H1sTyrLeuValTyrTrpGluArgGlnAlaGluAspSerGlu
p position: 6q23-6q24

perfamily: interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 alserAlaArgThrMetPro 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 LysArgArgSerLeuGluGluValGlyAsnValThrAlaThrThrProTh 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678 yLeuLysLeuProSerArgThrTrpSerProProPheGluSerAspAspS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  777 rLeuProAspPheProAsnIleSerSerThrIle.....AlaProThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  993 .....AAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 erGlnLysHisAsnGlnSerGluTyrAspAspSerAlaSerGluCysCys 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 erHisGluGluHisArgProPheGluLysValValAsnLysGluSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825 aCysAsnGlnAspSerProGluGluArgSerGlyVal...AlaAlaTyrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809 ValileSerGlyLeuArgHisPheThrGlyTyrArgIleGluLeuGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerCysProLysThrAspSerGlnIleLeuLysGluLeuGluGluSerSe 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGC 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTTACCTT...
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                                                                                                                                                                                                                                                                       PIDN: AAA52731.1;
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                                                                                                                PID:g306915
    10 - 20 - 20 min
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US-09-240-675-1 x A31555
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                                                                                                                                                                                                                                                    618 TATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGT 667
       167 CysTyrIleArgValTyrAsnVal.TyrValArgMetAsnGly.....S
                                                                       715 CTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTC..
                                                                                                                     181 erGluIleGlnTyrLysIleLeuThrGlnLysGluAspAspCysAspGlu
                                                                                                                                                  668 CTATAGTCCAGTAC...ATTGTATAAAGACCACAGTTGAAAATGAACTAC 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468
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                                                                                                                                                                                                                                                                                                                                                                                               147 sProSerValPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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C; Keywords: cytokine receptor; transmembrane protein

to: A31555 from: 1 to: 489 Percent Identity: 22.222 Length:

518 ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG 327 AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG 367 227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276 180 AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA 226 130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 179 568 AAAATÄTTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACT 113 rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP 277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 33 GTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATG 82 34 snValThrIleGluSerTyrAsnMetAsnProlleValTyrTrpGluTyr 50 17 aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA 34 83 GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA 129 1 MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17 CCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517 roLysLeuAspIleArgLysGluGluLysGlnIleMetIleAspIle... CAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT 467 GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC 417 TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy 113 nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH 82 isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu .....GlnIleMetProGlnValProValPheThrValGluValLysAs .....AsnGlyAspGluGlnGluValA .....TyrAspProGluThrThr 166 ...PheHi 147 567 160 145 98 65 617 130 326

4.1 FrovailbysphealaargpheprovalThrGlyLeuIleGluGlyArgSe 443	GAATGTTATGAAGAAATTAAATTG	TAAAATTGTCTGGGTGT		GAACAGG     ::::::   pLysGln	US-09-240-675-1 x 542167, from: 1 to: 1451	Percent Similarity: 45.652 Percent Identity: 19.783	Ly: 123	ferences: ily: skel	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1451 <viiv< th=""><th></th><th>es: Homo sapiens (ma 13-Jan-1995 #sequen sion: S42167 neier, U.; Obermann,</th><th>entatio</th><th>297 u 297 sec name: pir2:s42167</th><th>1047 T 1047</th><th>997 TIGATACIGAAATACAAGCTITCCTACTICCTGCAGTCTTTAACATTAGA 1046 ::::      :::::       :: 281 IleIleLeuProLysSerLeuIleSerValValArgSerAlaThrLeuG1 297</th><th>947 ACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAAAAAAGT 996 ::     </th><th>897 TGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGT 946    :::    </th><th></th><th>806 GTGGCTCCACGCCTTTTAAAAAGGAATCCTGGAAACCATT</th><th>214 sValSerAlaGluGlyValLeuHisValTrpG 225</th></viiv<>		es: Homo sapiens (ma 13-Jan-1995 #sequen sion: S42167 neier, U.; Obermann,	entatio	297 u 297 sec name: pir2:s42167	1047 T 1047	997 TIGATACIGAAATACAAGCTITCCTACTICCTGCAGTCTTTAACATTAGA 1046 ::::      :::::       :: 281 IleIleLeuProLysSerLeuIleSerValValArgSerAlaThrLeuG1 297	947 ACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAAAAAAGT 996 ::	897 TGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGT 946    :::		806 GTGGCTCCACGCCTTTTAAAAAGGAATCCTGGAAACCATT	214 sValSerAlaGluGlyValLeuHisValTrpG 225
ATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTG	1011 CAAGCTTTCCTACTTCCTCCA	961 GAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATA 1010 1:::::::::::::::::::::::::::::::::	911 AAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGGAATCTGATG 960	861 CAANTACCTGACTGTCAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCA 910 %	648. roCysAsnAsnAsnProVallysThrHisArgPhe	631. uValclyTyrTyrIleGluAlaAsnVallAlaGlySerGlyLysTrpGluP 648.	774 TATACATATGCAAACATGACCTTTCAAGTTCAGTTCC 813	747 AATCAGAACTATGTTCTTAAATGGGAT	702GAÑANTGAÑCTÂCCTCCACCAGAÑAATATAGAAGTCAGTGTCCAA 746	677 AGTACATTGTATAAAGACCACAGTT	627 AMAGTTAMAGCAGCACTACTTACGTCAMGGAMAMTTGGTGTCTATAGTCC 676 :::  :::::      :::      :::  574 ArgValArgCysSerAspSerAlaGlyValGlyGluPr 586	582 AGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626 [		578 TTCC	540	508 TAAGCTTTACA	458 ACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTT 507 ::::::::::::::::::::::::::::::::::::	408 ATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGAT 457 :::	369TATGAĞGTTĞAĞTĞTAÇAĞÇATTTAÇAĞÇATĞĞĞĞAĞĞĞĞÇAĞ 407	443 rTyrilePheArgValArgAlaValAsnLysMetGlyIleGlyPheProS 460

266 GARTATTACTAGTACC:	ALAGGAGGATGAOTCTGTCGGGAATGTCACTTC	105 GGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATA 149  105 GGAACAACTTA 11	Ouality: 118:00 Ratio: 0.602 nt Similarity: 42:795 ent_block: -240-675-1 x S51604	A;Note: the authors translated the codon GAC for residue 170 as Glu A;Note: the authors translated the codon GAC for residue 170 as Glu C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C;Reywords: ATP; transmembrane protein C;Reywords: ATP; transmembrane protein F;651-917/Domain: protein kinase homology <kin> F;659-667/Region: protein kinase ATP-binding motif</kin>	plexie, P.C.; Bar 8, 3277-3288, 19 Ehk-1 and Ehk-2: nnce number: S4901 ilon: S51604 :: preliminary ile type: mRNA les: 1-981 <aria les: 1-981 <aria< th=""><th>2:S51604  tion_block: tyrosine kinase Ehk-1 - rat this norvegicus (Norway rat) y-1995 #sequence_revision 21-Jul-1995 #te</th><th>1231 ATTGTGTGAAAGCCAGAGCACCACCATGAATGAAAAGCTGAATAAAAGC  </th><th>1143TTTTGGGAAACACTTCAAATGCTGAGAGAAAATTAT 1180                                      </th><th>:   :::      :::       :::            :::::      </th></aria<></aria 	2:S51604  tion_block: tyrosine kinase Ehk-1 - rat this norvegicus (Norway rat) y-1995 #sequence_revision 21-Jul-1995 #te	1231 ATTGTGTGAAAGCCAGAGCACCACCATGAATGAAAAGCTGAATAAAAGC	1143TTTTGGGAAACACTTCAAATGCTGAGAGAAAATTAT 1180	:   :::      :::       :::            :::::
:::::::::::::::::::::::::::::::::::::::	961 GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATA 1010 3::    436 1sThTASSTYTTHTPhe 1011 CAAGCTTTCCTACTCCTCCAGTCTTTAACATTAAGATCCCTTAGTGATTC 1060 3::    436 1sThTASSTYTTHTPHE 105	AAA nGI	771	720	648 ACGTCATGGAAAATTGGTGTCTATAGTCCAGTACAT	551 TGTAGAAGAAAGGATTGAAAATÄTTTATTCCAGACATAAAATTTATA 597	1 TAGT	351 GAAAACACTTCTTCATGGTÄTGAGGTTGACTCATTTACACCATTTCGCAA 400 :::::  :::: 252 AlaAspSerSerGlnLeuLeuGluValSerGlySerCysValAsnHisSe 268 401 AGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAA 450 :::	223 eAlaieuValSerValArgValTyrTyrLysLysCysProSerValValA 240 201 TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTÄTAAGAGCAGAAAAA 350

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455 yThrArgGlnTyrValSerValAsnValThrThrAsnGlnAlaAlaPros 472  1102 CGCCTGTGATCCAG	1233 TG 539 Va	1185 522 er	1136 AA    505 uI	1116 489 Le	1102 CG :: 472 er	455 YT
172 11115 188 188 1135 1135 1184 1184 1232 522 538	TGTGAAAGCCAGAGCACACACC 1256 :::       :::    lPheGlnIleArgAlaArgThr 546	AAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACTG	TTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAG. ]    :::::  ::: :::::::::::::::::::::::		CCTGTGATCCAG	hrArgGlnTyrValSerValAsnValThrThrAsnGlnAlaAlaProS 4
		1232	1184	1135 505	1115 188	172

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Database: SwissProt_38:*
Database sequences: 83857
Database length: 30454973
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Query length: 1343
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Query: US-09-240-675-1
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-DB-SW158FYCT_38 -QFMT-fastan -SUFFIX-modif_rsp -GAPOP-12.000
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-QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELOP-6.000 -DELEXT=7.000 -STAFT-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext|-MINLEN-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ssProt_38:CIC2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3SProt_38:PTPD_HUMAN + 116:00
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161.77
156.97 0
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135.94 0.3858
139.72 0.3913
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152.67 0.0476
148.19 0.0606
149.22 0.0701
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77 0.0140
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489 | P15260 homo sapiens (human)
1451 | P5279 homo sapiens (human)
1005 | P54757 rattus norvegicus (rat
575 | Q61727 mus musculus (mouse)
6 | 1372 | P15208 mus musculus (mouse)
6 | 1912 | P23468 homo sapiens (human)
1450 | Q02173 gallus gallus (chick
880 | P55146 rattus norvegicus (rat)
1447 | P70211 mus musculus (mouse)
1 | P54756 homo sapiens (human)
1 | P70875 homo sapiens (human)
1 | P78575 homo sapiens (human)
1 | P78575 homo sapiens (human)
1 | P54290 rattus norvegicus (rat
1 | P78575 homo sapiens (human)
1 | P54290 rattus norvegicus (rat
1 | P65213 homo sapiens (human)
1 | P54290 rattus norvegicus (rat
1 | P65213 homo sapiens (human)
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1 | P54270 | P54289 homo sapiens (human)
                                                                                                                                  1 P40189 homo sapiens (human) 1 P15261 mus musculus (mouse) 1 P08973 spinacia oleracea (si P56786 arabidopsis thaliana 1 P08575 homo sapiens (human) 1 P43811 haemophilus influenza 1 P32927 homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                   P42701 homo sapiens (human)
1 P26955 mus musculus (mouse)
1 P20241 drosophila melanogasi
1 P10586 homo sapiens (human)
1 P09976 nicotiana tabacum (d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 bos taurus (bovine
39 ovis aries (sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SwissProt_38:CA1C_CHICK
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                                                                                                                                                                                                                                                                         EMBL; J03171; AAAS2730.1;
EMBL; X60459; CAA42992.1;
PIR, A32694 A32694
PIR; S17112; S17112
MIM; 107450;
                                                                                                                                                                          SIGNAL
DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                     Phosphorylation
                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION BY TYK2. MEDLINE: 95059042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INR1_HUMAN
                                                                                                                                                                                                                                             Transmembrane; Glycoprotein; Signal; Polymorphism;
436
457
557
220
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seq_name: SwissProt_38:INR1_HUMAN
STANDARD;
                                                      97.50
97.50
97.50
97.50
                                                       137
125
124
116
                                                                                     P06242 saccharomyces
                                                                 P48356 mus musculus
P11722 callus
                                                  P11722 gallus gallus
P13944 gallus gallus
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SEQUENCE FROM N.A.

MEDLINE; 90124632.

Uze G., Lutfalla G., Gresser I.

"Genetic transfer of a function
into mouse cells: cloning and of the cell 60:225-234(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
MEDILINE; 92129376.
Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mullersman J., Witte M., Krishman K., Krolewski J.;
"Direct binding to and tyrosine phosphorylation of the alpha subunit
of the type I interferon receptor by pl35tyk2 tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colamonici O., Yan H., Domanski P.,
Mullersman J., Witte M., Krishnan K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-BUG-1990 (Rel. 15, Last sequence update)
115-FEB-2000 (Rel. 39, Last annotation update)
1NTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
                                                                                                                                                                                                                                                                                                                     SUBURITS THEMSELVES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES
EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.

FIM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYRO TYROSINE KIN
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONES TO THE CLASS II CYTOKINE FAMILY OF RECEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell. Biol. 14:8133-8142(1994).
FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE I TENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS. TYRZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           functional human interferon alpha receptor ng and expression of its cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Handa R., Smalley D
                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                  RECEPTORS.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.

INTERFERON-ALPHA/BETA RECEPTOR CHAIN.

527 ACTTATCTGGAAAACTCTTCAGGTGTAGAAAGAAAGAATGATATTT 576	427 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCCTGGAACA 476	327 AAATTGCGTATAAGAGCAGAAAAAGAAAACĀCTTCTTCATGGTATGAGGT 376	227 AACIGGGATGGATAAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276	127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176	7 AFGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTC	100.000 Percent Identity: 100.0 RR1_HUMAN from: 1 to: 557	SEQUENCE 557 AA; 63525 MW;  ignment_scores:     Quality: 2313.00     Ratio: 5.305	313 313 POTENTIAL. 314 314 POTENTIAL. 376 376 POTENTIAL. 416 416 POTENTIAL. 431 433 POTENTIAL. 433 433 POTENTIAL. 168 168 'L -> V. 177 177 177 177 177 177 177 177 177 177	MOD_RES 466 466 MOD_RES 481 481 CARBOHYD 50 50 CARBOHYD 58 58 CARBOHYD 81 81 CARBOHYD 81 88 CARBOHYD 110 110 CARBOHYD 172 172 CARBOHYD 172 172
						-			(उ.स.
01-OCT-1993 (Rel. 27, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)	hrsertys 436 SwissProt_38 SwissProt_38 Hentation_block 1_BOVIN STI 790;	AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAAC	384	roprovalpheAsmIleArgSerLeuSerAspSerPheHisIleTyrIle 350 roprovalpheAsmIleArgSerLeuSerAspSerPheHisIleTyrIle 350 GGTGCTCCAAAACAGTCTGGAAACAGGCTGTGATCCAGGATTATCCACT 112	927 GRAATTTACCTTCCGCGTACAAGCATCTGATGGAAATAACAATCTTT 976	SATGASNPTOGIYASNHISLEUTYTLYSTTPLYSGINIleProAspCysG AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA	777 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTAAA 826	677 AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726	577 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626

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alignment_scores:
alignment_block:
US-09-240-675-1 x INR1_BOVIN
                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a bovine alpha interferon receptor.";
"Cloning and characterization of a bovine alpha interferon receptor.";
"Cloning and characterization of a bovine alpha interferon receptor.";

Biochim. Biophys. Acta 1173:314-319(1993).

-I FUNCTION: RECEPTOR'FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFUS TRIGGERS TYROSINE PROTEINS AND IFU-R ALPHA-AND BETA-
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFU-R ALPHA-AND BETA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X68443; CAA48484.1;
EMBL; L06320; AAA02571.1;
PIR; S33770; S33770.
PIR; S27387; S27387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.; "Specific antiviral activities of the human alpha interferons are determined at the level of receptor (IFNAR) structure."; FEBS Lett. 313:255-259(1992).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovi
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SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS
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ATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020

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TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

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lePheProProValIleSerValLysSerValThrAspAspSerLeuHis TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGT...GATTCATTCCAT 1067 rSerPheTrpSerGluGluLysGluPheAsnThrGluMetLysThrIleI 332

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetariiodactyla; Ruminantia; Pecora; Bovoidea; Bovic
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                                                                                                                                                  Hank C. S., Mathialagan N., Klemann S.W., Roberts R.M.;
"Molecular cloning of ovine and bovine type I interferon receptor
subunits from uteri, and endometrial expression of messenger
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-ENDOMETRIUM;
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                                                                                        Endocrinology 138:4757-4767(1997) 24 UNS 15 WEST SEC. 1822 ( 12)
                                                                                                            ribonucleic acid for ovine receptors during the estrous cycle and pregnancy.
                                                                                                                                                                                                          MEDLINE; 98006426
                                                                                                                                                                                                                                                                                                        "Structure of an owine interferon receptor and its expression andometrium.";
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                                  FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
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TYPE I MEMBRANE PROTEIN
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US-09-240-675-1 x INR1\_SHEEP ....

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                                                                                                                 CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                  EMBL; U65978; AAB84231:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              DOMAIN
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 SEQUENCE
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               CONFLICT
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                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal BY SIMILARITY.
                                                        POTENTIAL.
POTENTIAL.
                            POTENTIAL.
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               A .->
                                                                                                                                             POTENTIAL.
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                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                          INTERFERON-ALPHA/BETA RECEPTOR
-> G (IN REF. 2).
-> D (IN REF. 2).
E7198A1905D4805C CRC64;
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                                                                                                                                                                                                                                                                                                          ALPHA
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280 CCAAATGCAACTTTTCTTCACTCAAGCTG...
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                                                                                                                                230 TGGGATGGATAATTGGATAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
                                                                                                  49 SerSerGluSerValArgAsnValThrPheSerAlaAspTyrGlnIleLe
                                                                                                                                                                                                                            130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                              32 snyalGluileHisIleileAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                      30. ATGGTCGTCCTCGGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCC
                                  65 uGlyThrAspAsnTrpLysLysLeuProGlyCysGlnHisIleThrSerS
                                                                                                                                                                                                                                                        16 gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLysSer...GluA
                                                                                                                                                                                                                                                                                            80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAATCTAAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                    1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr
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AATGTTTATGAAGAAATT 326
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921 CAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 rSerValValIleTrpLysAsnSerSerSerLeuGluGluArgThrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 TACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT...CCT 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                    TTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTG
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AGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAA
                                                                                                                                                  ValSerValSerAlaSerGluGluSerGluAsnMetSerValAsnGlnLe 365
                                                                                                                                                                                                 ATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGA 1117
                                                                                                                                                                                                                                                TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGT...GATTCATTCCAT
                                                                                                                                                                                                                                                                                                                                                                      ATCTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATAAAAGCTTTCC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                 SerMetGlyIleTyrTyrValArgValArgAlaSerAsnGlyAsnGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snCysGluAsnValThrThrThrHisCysValPheProArgAspIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGTGAAAATGTCAAAACTACCCAGTGTGTGTGTTTCCTCAAAACGTTTTC 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysLeuLysValLysAlaGluLeuArgLeuGlnSerArgValGlyCysTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATA 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA 373
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                                                                                                                                                                                                                                                                                                                                               rSerPheTrpSerGluGluLysGluPheAsnThrGluValLysProIleI
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                                          SEQUENCE
                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M89641;
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SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBLILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

TRANSMEM

Z

7EC6DFF370185D3A CRC64;

POTENTIAL:
POTENTIAL:

POTENTIAL. POTENTIAL.

CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.

POTENTIAL

AAA37890.1;

IFNAR

Glycoprotein; Signal.

INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN.
ENTRACELLULAR (POTENTIAL)

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seq_name: SwissProt_38:INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 roGlyAsnThrSerLys 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399
In homospecific or heterospecific background.";

Proc. Matl. Acad. Sci. U.S.A. 89:4774-4778(1992).

-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

-I- FUNCTION: TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

CHERITATE STRUCTURES.
                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 luArgLysValLeuGluLysArgThrAspPheThrPheProAsnLeuLys
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     FNAR1 OR IFNAR OR IFAR
                                                                                                                    Behavior of a cloned murine interferon alpha/beta n homospecific or heterospecific background.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gTrpAsnLysGlySerSerTyrSerAspThrValCysGluLysThrLysP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAA 1267
                                                                                                                                                                Lutfalla G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                        Bandu M.T., Proudhon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                           Mogensen
                                                                                                                                    receptor
                                                                                                                                                                                                                                                           Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                         (IFN-ALPHA-REC)
                                                                                                                                                        X.E.;
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alignment_block:
us-09-240-675-1 x INR1_MOUSE
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                                                                                                                                                                                                                                                                                                                 eArgIleTrpGlnLysSerSerSerAspLysLysThrIleAsnSerThrT
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                                                                                                                                                        GluValLysAlaIleHisProSerLeuLysLysHisSerAsnTyrSerTh
                                                                                                                   ATATÀGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT '776
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTATCTGGAAAAACTCTTCAGGTGTÁGAAGAAAGGATTGAAAATATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleAlaSerAlaAspValLeuPheArgAlaGlnTrpLeuProGlyTyrSe 267
                                       ...ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTT 823
                                                                              snLeuGlnValAspAlaGlnGlyLysSerTyrValLeuLysTrpAspTyr
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3.230
75.917
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Gaps: 4
Percent Identity: 48.624
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TISSUE-FETAL BRAIN;
MEDLINE; 93300510.
Lutfalla G., Gardiner K., U
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FCT-1996 (Rel. 34, Last.annotation update)
01-FCT-1996 (Rel. 34, Last.annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.

MEDLINE; 96054036.

MULTIFILE G., MCIDDIS M.G., Antonarak
"Structure of the human CRFB4 gene:
neighbor.";
MCI. Evol. 41:338-344(1995).

Antonarakis S.E.,

comparison with its

IFNAR

Uze G.;

Genomics 16:366-373(1993).

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"A new member of the cytokine receptor gene family maps on chromosome last than 35 kb from IFNAR.".

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alignment_scores:
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                                   357 ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                       260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
97 HisSerAspTrpValAsnIle ... ThrPheCysProValAspAspThrIl 112
                                                                                                           310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA. AAAGAAAAAC 35
                                                                                                                                                                                                                                                                                                                                        160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCTGGGGAATGTGACTTTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                  123 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
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EMBL; U08988; AAA86872.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch
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                                                                                                                                               sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS 80
                                                                                                                                                                                                                           ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                               TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                  yMetValProProCluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                           erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                          snIleLeuGlnTrpGluSerProAlaPhéAlaLysGlyAsnLeuThrPhe
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BY SIMILARITY.
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here are no restrictions on it
as its content is in no wa
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE ITN-GAMMA SIGNAL TRANSDUCTION PARHWAY AND IS LIKELY TO INTERACT. HITH GAF, JAKI, JAND/OR JAKE.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 rThrHisAspGluThrValPro 219
use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
1NTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
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Homo sapiens (Human).
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EMBL; U05875; AAA16955.1; EMBL; U05877; AAA16956.1; MIM; 147569; -.

Transmembrane; Glycoprotein; Signal; Repeat

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178 isTyrTrpGluLysGlyGlyLleGlnGlnValLysGlyProPhe 192	529 TTATCTGGAAAAACTCTTCAGGTGTAGAAAGAAAGAATTGAAAATATTTAT 578	eAlaAspThrSerThrAlaPhe	149 ThrproglyGluGlySerLeuIleIleArgpheSerSerPropheAgp11 165 479 AGATAGTGTBAGGCTTTGGATGGTTTAAGCTTTACATATAGCTTAC 528	478	148 THE OF SECTION	CACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTÄGÄÄ.	341 AGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTA 387	104 GlyPheProMetAspPheAsnValThrLeuArgLeuAr 116	300 CTCAAGCTGAAGGTTAATGAAGAAATTAAATTGCGTATAAG 340	205 AGAATAUTAGTAGTACCAAATGCAACTTTUCTICA SAA	Tippnetnialaspilemetseilegiyvalasniysi	GATGGATAATTGGATAAAATTGTCT	ArgProValValTyrArgValGlnPheLysTyrThrAspSerLys	42 snalagluginvalleuSerTrpGluproValAlaLeuSerAsnSerThr 58 183 GATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAAAACTGG 232	151 ATGACAACTTTATCCTGAGGTGGAACAGGAGC 182	108AAAAATCTAAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150::::::::::::::::::::::::::::::::::	60 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA 107 :::   ::: :::   :::::: :::	Align seg 1/1 to: INGS_HUMAN from: 1 to: 337	alignment_block: US-09-240-675-1 x INGS_HUMAN	Percent Similarity: 50.333 Percent Identity: 22.333	: 155.50 Length: 30	un) 0/034 MM, TOCOTOTOMOSOMOOD	VARIANT 64 64	CARBOHYD 137 CARBOHYD 219 CARBOHYD 231	FD 56 56 POTENTIAL: FD 85 85 POTENTIAL. FD 110 110 POTENTIAL.	DOMAIN 28 247 TRANSMEM 248 268 DOMAIN 269 337	∞
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EMBL; M29014; AAA41441.1;	n email to license@isb-sib.cl	~00	This SWISS-PROT entry is copyright. It is produced through a collaboration between. the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its		- 1- SUBCELLULAR LOCATION: TYPE I MEMBERANE PROTEIN - 1- SIMITARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE- PROTEIN KINASES.	BONDS, THE ALPHA CHAINS CONTRIBUTE TO THE PORMATION OF THE LIGAND- S BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.	- I- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE - IS SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHÂINS LINKED BY DISULFIDE	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.	့ ကွ	- 14 14 1	TOUT TOUT	"The rat insulin receptor: primary structure and conservation of tissue-specific alternative messenger RNA splicing.";	g I g		INSR.  Raftus porvedicus (Rat).	걸통진준	documentation_block: INSR_RAT STANDARD; PRT; 1383.AA. P15127: P97681;	name: SwissProt_38:INSR_RAT	757 ATGTTCTTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTTCAG 806 :::       :::   :::::: :::   :::::: 276 eulleLysTyTTpPheHisThrProProSerIleProLeuGlnIleGlu 292	259 uSerValLeuAlaGlyAlaCysPhePheLeuValLeuLysTyrArgGlyL 276	744	:::     :::      ThrGluLeuGlnGlnValIleLeuIleSerValGlyThrPheSerLeuLe	226 alGlyHisLeuSerAsnileSerCysTyrGluThrMetAlaAspAlaSer 242 711 CTACCTCCACCACAAAATATAGAAGTCAGTGTC	TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA	623 TCTAAAAGTTAAAGCACCACTACTTACGTCATGGAAAA 660	ArgSerAsnSerIleSerLeuAspAsnLeuLysProSerArgValTyrCy	579 TCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTG 622

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alignment_scores:
Quality:
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US-09-240-675-1
472 SerGlyThrLysGlyArgGlnGluArg.AsnAspIleAlaLeuLysThrA 488
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                             125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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MPORTANT FOR BIOLOGICAL ACTIVITY.
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AATTTACCTTCTCCGCGTACAAGCAT	AATGTCAAAACTACCCAGTGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGG	ATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAA	TGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAAGGA .::  - ::    .::  - ::    .::  - ::	GTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATA ASSSETSETSETGINILELELELLYSTTPLYSPTOPTOSETASPPTOAS	AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT	GTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAA	CTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCACCACTAC		targely GTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAA	GATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAG	TAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTT			D AGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCA	CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAA	2 GTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCA      ::    8 yrGlnAsnValThrGluPheAspGlyGlnAspAlaCys	OAspPheArgAspLeuLeuGlyPheMetLeuPheTyrLysGluAlaProT	ArgThrSerPheAspLysIleLeuLeuArgT	",	8 snglyAspGlnAlaSerCysGluAsnGluLeuLeuLysPheSerPheIle	
954 695	928 678	878 668	831 654	781 650	740 633	690 617	649	583	599 599	549	499 581	570	559	399	349	550	538		242	504	
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Eutheria; Primatės; Catarrhini; Hominid
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01-APR-1990 (Rél. 14, Last sequence update)
15-JUL-1999 (Rél. 38, Last amoutation update)
1NTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
Walter M.R., Windsor W.T.,
Zauodny P.J., Narula S.K.;
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                                                                                                                             K-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
                                                                                                                                                                                                                                             Stueber:D., Friedlein®A., Fountoulakis M., Lahm H.-W., 
*Alignment of disulfide bonds of the extracellular dome 
interferon; gamma: receptor and investigation of their ro 
idological activity.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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"Neutralizing epitopes on the extracellular interferon gamma receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 376:230-235(1995).
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                                                                            use by non-profit institutions as a constant is not removed. Usage by and fo modified and this statement is not removed. Usage by and formedified and this statement (See http://www.isb-sib.
                                                               entities requires a license agreement (
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EMBL; J03143; AAA52731.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol. 273:882-897(1997).
FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTOR'S BIND ONE
                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN:
FYM: PHOSPHORYLATED AT SER/THR RESIDUES.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CYTOPLASMIC (POTENTIAL). INTERFERON-GAMMA RECEPTOR ALPHA CHAIN. POTENTIAL. POTENTIAL. POTENTIAL EXTRACELLULAR (POTENTIAL) DCF9E574D8F47400 CRC64; of Bolance. 351 Ç.,

## alignment\_block: US-09-240-675-1 x INGR\_HUMAN Percent Similarity: 53.276 Length: 351 Gaps: 16 Percent Identity: 22:222

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- 33 GTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGGCCCATG 1 MethlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA 17 129
- 130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 17 aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA 179 4

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251 lValAlaAlaLeuLeuPheLeuValLeuSerLeuValPheIleCysP
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        281 IleIleLeuProLysSerLeuIleSérValValArgSerAlaThrLeuGl
                                                           997 TTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGA 1046
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                                                                                                                he.....TyrIleLysLysIleAsnProLeuLysGluLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vinkemeier U., Obermann W., Weber K., Fuerst D.O.;
"The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron microscopy of two titin-associated proteins.";
J. Cell Sci. 105:319-330(1993).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
MYOMESIN 1 (190 KD TITIN-ASSOCIATED PROTEIN)
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Muscle
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    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to license@isb-sib.ch).
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    162452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is not removed. Usarro
                                        FIBRONECTIN TYPE-III.
                                                                                                        FIBRONECTIN TYPE-III.
                                                                                 FIBRONECTIN TYPE-III
                                                                                                                            IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                            FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                FIBRONECTIN
                                                                                                                                                                                                                       G-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                                                                                                                                                                                                                                                                             AA TANDEM REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Thick filament; Repeat.
                                                                                                                                                                                                                                                              TYPE-III.
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CRC64;
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123.50 0.588

Length: Gaps:

alignment\_block: US-09-240-675-1 x MYM1\_HUMAN Align seg 1/1 to: MYM1\_HUMAN Percent Similarity: 45.652 Percent Identity: 19.783 153 GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAAT... 404 olleLeuGlyTyrPheIleAspLysCysGluValGlyThrAspSerTrp. 420 508 TAAGCTTTACA......TATAGCTTACTTATCTGGAAA... 539 477 LeuLysSerPro.....LeuSerThrLeuAspTrpThrValIleVa 460 erArgValSerGluAlaValAlaAlaLeuAspProAlaGluLysAlaArg 369 .....TATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAG 407 443 rTyrIlePheArgValArgAlaValAsnLysMetGlyIleGlyPheProS 460 333 .....CGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGG: ... 368 427 ProValLysPheAlaArgPheProValThrGlyLeuIleGluGlyArgSe 297 TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTG...... 247 TAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCT 296 201 .... GTGACTTTTTCATTCGATTATCAAAAAACTGGGATGGATAATTGGA 246 388 AspTyrileIleIleSerTrpLysGlnProAlaValAspGlyGlySerPr 404 582 ....AGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626 540 uAlaGlyThrGluAsnTrpGlnArgValAsnThrGluLeuProValLysS 557 524. ProGlyGlnArgGlyHisGluGlyIleMetTyrPheValGluLysCysGl-540 540 ..... AACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTA 577 490 lThrGluGluFroSerGluGlyIleValProGlyProProThrAspl 507 458 ACACATCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTT 603.ysAlaProGlyLysIleIleProSerArgAsnThrAspThrSerVal... 618 574 ArgValArgCys.....SerAsnSerAlaGlyValGlyGluPr 586 627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676 557 erProArgPheAlaLeuPheAspLeuAlaGluGlyLysSerTyrCysPhe 573 702 .....GARAATGAACTACCTCCACCAGAAATATAGAAGTCAGTGTCCAA 746 .....SerGlnCysAsnAspThr 426 euSerValThrGluAlaThrArgSerTyrValValLeuSerTrpLysPro 523 ATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGAT AGTACATTGTATAAAGACCACAGTT..... oSerGluAlaThrGluValThrValValGlyAspLySLeuAspIleProL 603 .TATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCC 813 332 701 490 457 476 443 507 たべ こび カーシベニー

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95206467. ., Pfarr S., Mi	SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN:	7-3288(1993).	with Aighterive structures and neuronal e	777.	SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY: TISSUE-BRAIN:	; Sciurognathi; Muridae; Murinae;	aryota; Metazoa; Chordata; Craniata; Vertebrata	,	INASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1).	5 PRECURSOR (	1-0CT-1996 (Rel. 34, L	Cor 1996 (Rel. 34, Created)	EPAS RAT STANDARD; PRT; 1005 AA.	Dame: SWISSPTOT_36:EFA3_KAI			1281 AGTGTTTTTAGTGACGCTGTATGTGAGAAA 1310	774 YrGlnPheGlnValAlaAlaMetAsnMetAlaGlyLeuGlyAlaProSer 7		758 lArgGluGluAlaTyrLysIleSerAsnLeuLysGluAsnMetValT 7	GTTCCTAATTTGAAACCACTGACTGTAT	745 GlyValProGlyLysTrpArgGluAlaAsnValLysAlaVa 7	האנה האמינים לאנים היים האמינים האנים האנים לאנים האנים  1096 GAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATT 1   :::::: :::	711 uSerPheArgAspSerMetValLeuGlyTrpLysGlnProAspLysThrG	ンボーン・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	Oll CARGCTTCCTACTCCTCCA	laAlaGlyLeuSerGluTyrSerGlnAspSerGluAlaIleGluVal	GAAGAGATAAAGTTTGATACTGAAATA	670		660ThrCysHisGlyLeuValThrGlyGlnSer 6	AATGTCAAAACTACCCAGTGTGTCTTTCCTCA	814 AGCCTTTTAAAAAGGAATCCTGAAACCTTTCTTAAATGGAAA 8 :: :: ::::::::::::::::::::::::::	uValGlyTyrTyrIleGluAlaAsnValAlaGlySerGlyLysTrpGluP	
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HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                he European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuroscience 63:163-178(1994
                                                                                                                                                                                                                    DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
                                                                                                                                                                                                                                                                                                                                       438
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              Å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase; ATP-binding; Phosphorylation;
e: Glycoprotein; Signal; Alternative splicing
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VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN TYPE-A RECEPTOR 5. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                            RESDPFIMACTR -> G (IN SPLICED FORMS
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(BY SIMILARITY).
(BY SIMILARITY).
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MBL outstation -
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369	353 hrMetAlaCysThrArgProProSerAlaProArgAsnAlaIleSerAsn	
740	720CCAGAAAATATAGAAGTCAGT	
353	rSerCysyalCysGluLysAspTyrPheArgArgGluSerAspProProT	
710	TOTATA A A CAPTA C	
683	AATTGGTGTGTATAGTCCAGTACAT	
326	ysAlaSerProHisserGlnThrCysSerLysCysProPro	
647	598 AACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTT	
313	yTyrGluGluLysAsnGlyThrCysGlnValCysArgProGlyPhePheL	
597	TOTAGAAGAAAGGATTGAAAATATT, TATTCCAGACATAAAATTTATA	
296	Tysalac	
л . V	THE ACCUPATION OF THE PROPERTY	
500	TAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTG	
285	268 rValThrAspAspProProLysMetHisCysSerAlaGluGlyGluTrpL	
450		
268	252 AlaAspSerSerGlnLeuLeuGluValSerGlySerCysValAsnHisSe	
400	CACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCA	
251	240 rgHisLeuAlaValPheProAspThrIleThrGly	
350	GTTTATGAAGAAATTAAAT	
240	223 eAlaLeuvalServalArgValTyrTyrLysLysCysProSerValValA	
300	CAAATGCA	
223	215 AlaPheGlnAspValGlyAlaCysIl	
265	GGAT	
214	198 snThrGluValArgAspValGlyProLeuSerLysLysGlyPheTyrLeu	
215	GATGAGTCTGTCG	
198	> `	
174	GACAACTIT	
183	100 GAMAMARICITGARANGITAGAGIRGAGATGATA	
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-	allgament_block: US-09-240-675-1 x Epa5 RAT	
	Percent Similarity: 42.795 Percent Identity: 20.087	
	ty: 118.00 Length: 45	

741 GTCCAAAATCAGAACTATGTTCTTAAATGG..

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seq_name: SwissProt_38:I10R_MOUSE
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                                                    HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.; A receptor for interleukin 10 is related to interferon receptors Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                 STRAIN-C57BL/6 X AJ F1; PTISSUE-HEMATOPOIETIC;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    INTERLEUKIN-10 RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                      15-JUL-1998
15-DEC-1998
                                                                                                                 EDLINE; 94068585
                                                                                                                                                                                                                                                  L10RA OR IL10R.
                                                                                                                                                                                                                                                                                                                           5-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                   OR MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValPheGinIleArgAlaArgThr 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erLysGluThrThrIleThrAlaGluGlyLeuLysProAlaSerValTyr 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCCATATCTATATCGGT......GCTCCAAAACAGTCTGGAAACA 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuSerTrpGlnGluProAspArgProAsnGlyIleIleLeuGluTyrGl 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAG. 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yThrArgGlnTyrValSerValAsnValThrThrAsnGlnAlaAlaProS
                                    FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                    (Rel. 37, Last sequence update) (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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FAMILY OF RECEPTORS. - 0 8-
                                                                                                                                                                                 Mammalia;
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the European Bioinformatics Institute
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                                      ...ValAspGluValIleLeu
                                                                                                                                                     TACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAG 435
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ROCOGEDADA
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                                                                                                                                                                                                                                                                                                                 334 erGlnPheLeuLeuPro 339
                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14; Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INSULIN RECEPTOR PRECURSOR (EC 2.7.1:112) (IR)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
[1]
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        110 Con 34
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MGD; MGI:96575; INSR.
MGD; MGI:96575; INSR.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00109; TYRRINASE.

PROSITE; PS00107; PROTEIN_KINASE_MTP; 1.

PROSITE; PS00109; PROTEIN_KINASE_MTP; 1.

PROSITE; PS00109; RECEPTOR_TYRASE_MTP; 1.

PROSITE; PS00119; RECEPTOR_TYRASE_MOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_MOM; 1.

PROM; PF00069; PKINASE; 1.

PFAM; PF00757; Furit-11ke; 1.

PFAM; PF01030; Recep_L_domain; 1.
                                                                                                                                                          NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00757; Furin-like; 1. PFAM; PF01030; Recep_L_domain; 1. PF01030; Recep_L_domain; 1. PF01030; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.
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MEDILINE; 90099338.

Sibley E., Kastelic T., Kelly T.J., Lane M.D.;

"Characterization of the mouse insulin receptor ger

Proc. Natl. Acad. Sci. U.S.A. 86:9732-9736(1999).

"In FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS a
                                                                           DISULFID
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                 TRANSMEM
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EMBL; M28869; AAA39319.1; -
PIR; A34157; A34157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. ...
use. by non-profit institutions as lone
modified and this statement is not remove
entitles requires a license agreement (so
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINASE ACTIVITY.

-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.

-I- ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES THE KINASE
                                                                                                                                                                                                                                                                       DOMAIN .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase. Kinetic correlation to autophosphorylation in the beta subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Substrate phosphorylation catalyzed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASES
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                                                                                                                                                                                                                                                                                  1372 AND CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSULIN RECEPTOR, ALPHA-SUBUNIT REMOVED IN MATURE FORM.
INSULIN RECEPTOR, BETA-SUBUNIT.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             institute. There are no resutions as long as its content is not removed. Usage by A
                                                                                                                                                                                                               POTENTIAL.
CYTOPIASNIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                PROTEIN KINASE.
ATP (BY SIMILARITY)...
                                                                                                              BY SIMILARITY: PHOSPHORILATION (AUTO-).
IMPORTANT FOR BIOLOGICAL ACTIVITY
                                                       POTENTIAL.
                                                                                                   BY SIMILARITY
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  600 CTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTAC 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 GTCAGAATATTACT.....AGTACCAAATGCAACTTTTCTTCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 ArgThrSerPheAspLysIleLeuLeuArgTrpGluProTyrTrpProPr 522
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                                                                                                                                                                                                                                                                                561 ......IleAspProProGln......ArgSerAsnAspProLys 571
                                                                                                                                                                                                                                                                                                                                                               350 AGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAA, 349
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                                                                                                                                     582 targGly.....
                                                                                                                                                                   500 GGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAG 549
                                                                                                                                                                                                      450 ATAGTGATACACATCTCCTCGGAACAAAAGATAGTGTTATGTGGGCTTT 499
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ID PTPD_HUMAN STANDARD; PRT; 1912 AA

AC P23468;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1996 (Rel. 34, Last sequence update)
                                                                                                            seq_name: Swissprot_38: PTPD_HUMAN
                                                                                                                                                                                                                                   810 IleGluLeuGlnAlaCysAsnGlnAspSerProAspGluArgCysSerVa
                                                                                                                                                                                                                                                     1236, GTGABAGCCAGAGCACACCATGGATGAAAAGCTGAATAAAAGCAGTGT 1285
                                                                                                                                                                                                1286 TITTAGTGACGCTGTATGTGAGAAAACAAAACCA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                         1145 TIGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAA ...... 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101 ACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTÄTTT 1144
                                                                                                                                                                                                                                                                                                            793 snLysGluSerLeuvalIleSerGlyLeuArgHisPheThrGlyTyrArg 809
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                                                                                                                                                         826 1 AlahlaTyrValSerAlaArgThrMetPro 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 AsnSerSerSerGlnIleIleLeuLysTrpLysProProSerAspProAs 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 729 rPheArg...LysThrPheGluAspTyrLeuHisAsnValValPheValP 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaThThTLeuThTLeuProAspPheProAshValSerSerThTlleVa 778
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                                                                 1912 AA.
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(35) (3) (3) (4)

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EMBL; 138929; AAC41749.1;
EMBL; X54133; CAA38068.1;
PIR; S12052; S12052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute, use by non-profit institutions as modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00102; Y_phosphatase;
Hydrolase; Receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS5005
PROSITE; PS5005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an
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'Structural diversity and
'yrosine phosphatases.";
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                                                                                                                                                                                                                                                                                                                           RANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 270:6722-6728(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
TISSUES DUE TO ALTERNATIVE SPLICING.
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
FROM THE TRANSMEMBRANE SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: PROTEIN TYROSI PROTEIN TYROSINE + ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS)
CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                             on 1265/Cites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; TYR_PHOSPHATASE_2; 2.
5; TYR_PHOSPHATASE_PTP;
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                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR" (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                PROTEIN-TYROSINE PHOSPHATASE DELTA.
                                                                                                                                       FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                               G-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                     TOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane protein-tyrosine
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                                                                                                                                                                                                   C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             There are no
                                                                                                              TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Duplication;
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	MW; 3AE8CBCD32182E26 CRC64;	AA; 214759		SEQUENCE	So
CLEAVAG	.5-FO	1178	1178	MUTAGEN	4
ORM)	(IN FETAL B	1137	609	VARSPLIC	Ŧ
	(IN KIDNEY	783	775	VARSPLIC	4
	•	229	226	VARSPLIC	1
-	MISSING (IN KIDNEY ISOFORM)	. 189	181	VARSPLIC	Ţ
	POTENTIAL.	832	832	CARBOHYD	1
	POTENTIAL.	724	724	CARBOHYD	T
	POTENTIAL.	299	299	CARBOHYD	H
4	POTENTIAL.	254	254	CARBOHYD	H
	CLEAVAGE (POTENTIAL)	1178	1175	SITE	Ŧ
	BY SIMILARITY.	1844	1844	ACT_SITE	L
	BY SIMILARITY.	1553	1553	ACT_SITE	Ţ
	PROTEIN-TYROSINE PHOSPHATASE	1912	1619	DOMAIN.	Ŧ
	PROTEIN-TYROSINE PHOSPHATASE	1618	1375	DOMAIN	Ŧ
	FIBRONECTIN TYPE-III	1137	1020	DOMAIN	FT

## alignment\_scores: US-09-240-675-1 x PTPD\_HUMAN Percent Similarity: 116.00 0.768 52.982 Percen.

Align seg 1/1 to: PTPD\_HUMAN 537 AAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATT...TATTCCAG 583 from: 1

775 ATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTA 824

luPro....GluGluProAsnGlyGlnIleGlnGlyTyrArgValTyrTyr 455

.HisasnvalalaaspSerGlnIleThrThrIleGlyAsnLeuValProG AAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCT 974 485

485, inLysThrTyrSerValLysValLeuAlaPheThrSerIleGlyAspGly 501

502 ProLeuSerSerAspIleGlnValIleThrGlnThrGlyValProGlyGl 518 TTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACT 102

3.40

425 26 21.647

183

378

411 227 395

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1125 CTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAA 1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545 AlaAsnTyrGluLeuValTyrLysAspGlyGluHisGlyGluGluGlnAr 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 AlaSerThrAlaGluIleSerAlaArgThrMetGlnSerLys.....Pr 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken):
Gallus gains (Chicken):
Eukaryota; Metazoa; Chordata; Crantata, Vertebrata; Archos
Phastaninae; Galliformes; Phastanidae; Phastaninae; Gallus
                                                                                                                                    EMBL; D11474; BAA02033.1;
PIR; A44027; A44027.
HSSP; P56276; lTLK
                                                                                                                                                                                                                                                 use by non-profit institutions as long as it modified and this statement is not removed. Usage entitles requires a license agreement (see http://
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE
-1- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDLINE: 93015907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PROTEIN, STRIATED MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
5-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete primary structure and tissue expression of chicken ectoralis M-protein.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE-FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSUE-EMBRYONIC PECTORALIS MUSCLE;
                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMENT REACHED ITS PEAK AFTER HATCHING.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE COMAINS.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA 1276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iol: Chem. 267:20302-20310(1992).
FUNCTION: IS A STRUCTURAL CONSTITUENT OF MYOFIBRILLAR M-BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_38:MPSF_CHICK
                                                                                           PF0004
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FENTYPEIII.
Repeat; Immunoglobulin domain.
238 - GIG-LIKE C2-TYPE DOMAIN.
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US-09-240-675-1 x MPSF_CHICK
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                                                                   520 spProProValProArgGlyArgGluProLeuThrTyrPheIleGluLys
                                                                                                                   538 AAAAC.
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                                                                                                                                                       rasnvalHisalaserGluIleSerLysThrTyrvalValLeuSerTrpa
                                                                                                                                                                                                                                                                                                                                                                              CANTAGTGATACACATCTCTCCTGGA.....ACAAAAGAT
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496
                            .TCTTCAGGTGTAGAAGGAAAGGATTGAAAATATTTATTCC..
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0.618
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FIBRONECTIN TYPE-III:
IG-LIKE C2-TYPE DOMAIN:
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seq_name: SwissProt_38:TYO3_RAT
MEDLINE; 96104999.
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TYO3_RAT STAND
                                                                                                                                                                                                                                                                                                                 1097 AAACACGCCTGTGATCCAGGATTAT 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633
              SEQUENCE FROM N.A. TISSUE-BRAIN;
                                                                   Rattus norvegicus (Rat), Alegaria (Particular de la Companyota; Metazoa; Chordata; Crantata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    924 AAAGGA...ATTTACCTTCTCCGCGTACAAGCATCTGATGGA.....
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                                                                                                                                                                                                                                                                                            726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       774 TATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616 alvalvalGlnTrpAspLysProLysHisGluGluAsnLeuTyrGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 583
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                                                           Eutheria; Rodentia;
                                                                                                                                    TYROSINE-PROTEIN KINASE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 AAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553 lLysSerProArgTyrAlaValPheAspLeuAlaGluGlyLysProTyrV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 SerMetValGlySerGlySerTrpGlnArgValAsnAlaGlnValAlaVa 553
                                                                                                                                                                               OCT-1996 (Rel: 34) Created) The suffer Assume Liber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrGlyGluGlnTyrilePheArgValLysAlaValAsnAlaValGlyPh
                                                                                                                                                                                                                                                                                                                                               CysAspGlyHisSerMetThrLeuGlyTrpLysAlaProLysTyrSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrIleAspTyrSerValValGlySerAsnGlnTrp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alPheArgVal.....LeuSerAlaAsnLysHisGlyIleSer 582
                                                                                                                                                                                                                                                                                    yGlySerProlleLeuGlyTyrTyr, 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eSerGluAsnSerGlnGluSerGluAlaIleLys......valG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTA.....
                                                                                                                                                                                                                                                                                                                                                                          GATTCATTCCATATCTATATCGGT.....GCTCCAAAACAGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                              lnAlaAlaLeuThrCysProSerTyrProHisGlyIleThrLeuLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . AATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AsnTyrAsnArg......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ......GluProAlaAsnHis......LysProIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lProSerAlaProGlyArgValValAlaThrArgAsnThrLysThrSerV 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .CCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAAT.....CAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspProSerGluIleThrGluProIleGlnProGlnAspIleValValVa 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTAT 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AGACATAAAATTTATAAACTCTCACCAGAGACTACTTATT 621
                                                                                                                                                                                                            STANDARD; PRT; 880 AA.
                                                       Chordata; Cran
Sciurognathi;
                                                                                                                                                    Last sequence update)
                                                                                                                                 TYRO3 PRECURSOR (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheValValHisGlyLeuGlu
                                                         Muridae;
                                                                                                                                                                                                                                                                                                                   Carried Control
                                                         Murinae;
                                                                                                                                                            1,45 G 1 Page 1
                                                      Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                  726
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    376-556-60-5
       The Comment of
                                                                                                                                                                                                           alignment_scores:
                                                                                                                                              Percent Similarity:
                                                                                                               US-09-240=675-1:x TY03_RAT:
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                            γ: 113.50
γ: 0 7.
                                                                                                                                                            45.634
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00107; PROTEIN KINASE ATP;
PROSITE: PS00109; PROTEIN KINASE TYR;
PROSITE: PS50011; PROTEIN KINASE DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D37880; BAA07119.1; - HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor tyrosine kinase.
J. Biochem. 117:1267-127:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohashi K., Honda S., Ichinomiya N., Nakamur, "Molecular cloning and in situ localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTI
IN THE CENTRAL NERVOUS SYSTEM.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 1267-1275 (1995) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein kinase; ATP-binding
  ž
                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                POTENTIAL
                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III: FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR
                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                         PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura
E86AAE5FA5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 T.,
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Align seg'1/1 to: TYO3\_RAT from: 1 to: 880

Percent Identity: 22.254 

Length:

15 LeuLeuLeuAlaGlyLeuAlaSerLeuLeuLeuProGly...... GTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATG 82 27

(b) (v) (c) (c)

GGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAG 132

942	893 CCAGTGTGTCTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCC
271	258GluTrpGluAlaLeuAlaValValValProValProProPh
892	TGACTGTGAAAATGTCAAAA
257	ి గ
247	nAlaSerValAlaTryValProGlyAlaAspGlyLeuAlaLeuLeuHisS
792	CTTAAATGGGATTATACATATGCAAACATGA
754 230	714 CCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAA
213	
713	GTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTA
213	TACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTG GPTOAlaIleIleArgLeuGlnAla
205	ThrGluPheSerCysGluAlaHisAsnIleLysGlyLeuAlaThrSerAr
613	TTATAAACTCTCACCAGAGAC
563 188	GGAAAAACTCTTCAGGTGTAGAAGAAAGG     ::::      \\\\\\\\\\\\\\\\\\\\\\\\\
175	Alas
158	PheGlnLeuSerCysGluAlaValGlyProProGluPr
478	AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAA
428 145	384TITACACCATTICGCAAAGCTCAGATIGGTCCTCCAGAAGTACAT
129	118SerGlnSerValTrpLeuThrValGluGlyValP
	03 GlyLeuTyrTrpCysGlnValLysAspGlyGluGluThrLysIle
337 <sub>?</sub>	8 AACTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTAT
287 102	238 ATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGC
86	nAsnAlaSerGlnValSerIleSerIleSerGluGln
237	CTTTTTCATTCGATTATCAAAAAACTGGGATGG
196 74	147 ATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGG :::
146.	133 TA
* 3	

943	271
GCGTACAAGCATCTGAT	eThrCysLeuLeu
TGGAAATAACACATC	ArgAsnLeuAlaPro
943 GCGTACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATA 992	271 eThrCysLeuLeuArgAsnLeuAlaProAlaThrAsnTyrSerLeuA 287
992	A 287

yProSerProTyrGlyAspTrpVal 303

<sup>993</sup> AAGTITGATACTGAA 1007 | [|-:::|||::: 304 PropheGlnThrLys 308

OM of: US-09-240-675-1 to:

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# 115.50 156.1
# 115.50 156.1
# 115.00 129.8
# sp_vertebrate:09W675 + 113.50 155.4
# sp_invertebrate:024495 + 113.00 155.4
# sp_invertebrate:024495 + 113.00 155.4
                                             sp_rodent:062682
sp_mamma1:077773
sp_rodent:054711
sp_rodent:088307
                                                                                                                         sp_invertebrate
sp_numan:095646
                                                                                                                                                                                                                                                                                                                                                                                                             sp_vertebrate:Q07784 + 117
sp_invertebrate:P91767 + 11
sp_invertebrate:Q09946 + 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_vertebrate:Q9YHW0 + sp_rodent.oction
                                                                                                                                                                                                                                                                            sp_invertebrate:Q230;
sp_invertebrate:Q235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_human:Q92673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database sequences:
Database length: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search information bloc
Query: US-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     About:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: Jun 1, 2000 6:02 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p_rodent:997798 + 13
p_invertebrate:Q94537 +
p_invertebrate:Q94538 +
p_vertebrate:Q90610 + 12
p_vertebrate:Q98949 + 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAXLEN-1000000 -USER-US0924067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB-SPTREMBL_12 -QFMT-fastan
                                                                                                                                                                                                                      _rodent:Q63155
                                                                                                                                                                                                                                                        invertebrate: Q235
                                                                                                                                                                                                  human:060469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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5.50 162.46 0.06
50 156.12 0.0693
00 129.83 0.1033
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                                                                                 6 0.22
0.2228
0.2688
0.2688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 1 Q94537 drosopl
26 1 Q94538 drosopl
1 Q90610 gallus gr
                                                                                                                                                                                                                                                7 | Q24495 drosophila melano

1 | Q64604 r protein-tyrosine |

8 | Q23020 caenorhabditis ele

1 | Q23550 caenorhabditis ele

0 | Q23551 caenorhabditis ele
                                                                                                                                                   Q63155 rattus norvegicus (ra
O60469 homo sapiens (human)
O60468 homo sapiens (human)
Q95209 oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                       P97603 rattus norvegicus (ra
                                                                             062682 rattus norvegicus (rat
062682 rattus norvegicus (rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 homo sapiens
140 homo sapiens
162 xenopus laevis
17859 caenorhabdii
                                                                                                                                                                                                                                                                                                                                                 166 homo sapiens
75 brachydanio re
                                                                                                                                                                                                                                                                                                                                                                                                   gallus gallus (chicken
767 manduca sexta (toba
46 caenorhabditis eléga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gallus ga
9 homo sap
                                                                                                                                                                                                                                  sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              la melanog
lus (chick
                                                                           (p1g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_invertebrate: 009165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
TTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGAT 443
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: sp_vertebrate:Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p_invertebrate:0612
                                            "Comparative genomic analysis of the receptor gene cluster."; Genome Res. 0:0-0(1999).
                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAY-1999 (TrEMBLrel. 10, Last ann
                                      EMBL; AF082664; AAD13669.1; -
                                                                                                                                                                                             Eukaryota; Metazoa; Chorc
Neognathae; Galliformes;
                                                                                                                                                                                                                                      Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                             INTERFERON ALPHA/BETA RECEPTOR
569 AA; 64055 MW;
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                               Phasianidae;
                                                                                                                                                                                                                 Craniata;
  F99BC099 CRC32;
                                                                                             UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                  569 AA
                                                                                                                                                                                             Phasianinae;
                                                                                                                                                                                                                 Vertebrata; Archosauria; Aves;
                                                                                                                                                                                               Gallus
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240-675-1 x Q9YHW0 691.50 2.384 63.736 from: Percent Identity: 37.363

Align seg 1/1 to: Q9YHW0

0		11
393	347 AAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCAT	34
113	97 SerAlaIleThrAlaTyrTyrAspThrHisHisIleArgIleArgAlaGl	
 346		: , ;29
 , 96	80 ysGluLeuSerGlyCysGlnAsnValSerHisThrGluCysAspPheSer. 96	60
296	247 TAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCT	24
8	63 rAlaGlnTyrGlnCysPheAspAspLeuGlnThrSerGluProGluTrpL	6
246		<u>بر</u>
63		
  211	162 ATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTC	16
 47	31.snLeuLysSerProGlnAspIleGlnValTyrAlaValAsnThrAsnPhe	ر در در
 161		. <b></b>
31		٠ <b>٠</b> <b>١</b>
111	62 GCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAA	
18	6 CysAlaSerGlyArgLeuAlaAlaValLeuLeuCysVa	
	12 TGCGGCGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGT	· ,
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1067 TATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1117 ATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCT 1166
                                                                                                                               1208 TAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 aThrValProLeuGluAspLysGlyGlyLeuPheSerProIleHisCysI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 spAsnSerSerAsnVal...GluLysValArgSerIleLeuProIleAsp 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 sMetTrp...LeuIleSerValPhePheLysTyrAsnValValIleTrpA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 yrGluIleAlaGlnIleGlyProProGluIleAlaLeuGlnSerIleAsn 146
                                                                                                                                                                                                                                                                   374 euTyrAspPheSerTyrGlnIleLeuTyrTrpLysAsnSerSerAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 erLysSerCysLeuSerLysAspValGluValAspProProValThrAsn 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        967 ACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         832 ATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAAT 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 leLysThrhrArgLysValAsnAspLeuLeuCysProThrAsnValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  688 TAPAGACCACAGTTGAA...AATGAACTACCTCCACCAGAAAATATAGAA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 ValileAsnAspLeuAlaProGluThrThrTyrCysLeuLysValGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 AAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 GlyAlaIleLysIleAsnIleSerProProGluAlaAsnGlnValArgLy 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 AAGGCAATAGTGATACACATCTCCTGGAACAAAAGATAGTGTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             917 TTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 IleThrSerMetLysCysAsnLeuSerSerVallleLysProThrSer.. 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 euTyrAspAspTyrSerSerLysTrpGlnLysValSerGlyCysGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 nGluH1sValThrTyrThrValGlnTyrLeuThrGlyTyrLeuLysAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   783 .GCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 ValPheAlaLeuAsnMetLysPheTyrLeuLeuTrpAspAsnHisTyrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          735 GTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATAT.. 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAGAAAAATTATCGAGAAAAAAACTGAT.....GTTACAGTTCC 1207
                                                                               rAspLeuAlaProSerThrLeuTyrCysValLysValGlnAla..... 422
                                                                                                                                                                                 GluGluGluValLysMetLysGluThrLysGlnThrIleAlaThrValSe 407
                                                                                                                                                                                                                                                                                                                                                                                sileLysileThrProProGlyGlyProGlyAsnLysileMetSerAspl 374
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Mar 16 . 17 . 1845
     122 rLeuAlaGluSerLeuHisLeuArgPheSerAlaPro...GlnIleGluA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_rodent:Q61190
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US-09-240-675-1 x Q61190
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                                                                                                                                                                                              90 rgAlaGluLeuAlaAspGluHisSerGluTrp...valAsnValThrPhe 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
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                                                    1049 CCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAA 1098
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                                                                                                                                              999 GATACTGAAATACAAGCTTTCCTACTTCCTACAGTCTTTAACATTAGATC
                                                                                                                                                                                                                                                           949 AAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTT 998
                                                                                                                                                                                                                                                                                                                                                          899 TGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761 TCTTAAATGGGAT.....TATACATATGCAAACATGACCTTTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last seg
01-NOV-1999 (TIEMBLIEL. 12, Last and
CYTOKINE RECEPTOR FAMILY 2, MEMBER 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 GlyThrAlaGlyGly 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 heSerGluAlaTyrAsnLysSerSerAspPheSerArgGluGluCysIle 438
                                                                                                         106 CysProValGluAspThrIleIleGlyProProGluMetGlnIleGluSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U53696; AAC53062.1; -. MGD; MGI:109380; II10rb. PFAM; PFO0041; FR3; 1. SEQUENCE 349 AA; 39774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIBBS V.C., PENNICA D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 97199375.
                                                                                                                                                                                                                                                                                                   74 SASpPhe...SerHisLeuSerLysTyrGlyAspTyrThrValArgValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                       58 SerTyrArgSerPheGlnAspHisCysLysArgThrAlaSerThrGlnCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGGAAACAAATACCTGAC...TGTGAAAATGTCAAAACTACCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTAT, 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolation of cDNA clones encoding the human and mouse
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1.660
62.617
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Gaps: 9
Percent Identity: 26.168
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Last annotation update)
MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
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898

801

760

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seq_documentation_block:
Align seg 1/1 to: Q63953 from: 1
                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                             EMBL; U69595;
EMBL; U69596;
EMBL; U69597;
EMBL; U69598;
EMBL; S69336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1137 ...ATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGA 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 ArgValGlnTyrTrpLysAsnGlyThrAsnGluLysPheGlnValValSe 171
                                                                                                                                                                                                                                                                                                                                                                                                            *Genomic organization and promoter analysis of the gene inngraencoding the second chain of the mouse interferon gamma recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 GluTrpSerGluProIleCysGluArgThr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unctionality of the murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A. EDLINE; 94170381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERFERON GAMMA RECEPTOR
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-NOV-1996 (Trembirel.
-NOV-1999 (Trembirel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 76:803-810(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rProTyrAspSerGluValLeuArgAsnLeuGluProTrpThrThrTyrC
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                                                                                                                                                                                                                                                 MGI:107654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rodent:Q63953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEMBIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodentia; Sciurognathi;
                                              x Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHEE S., MUTHUKUMARAN G., LEMBO D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., STARK G:, DI MARCO F., AGUET M.; f the interferon receptor family complements
                                                                                                                                                                                                             37471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                            63. 15.
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12, Last annotation update
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                                                                                               Gaps:
Percent Identity:
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                                                                                                                                                                            THE COURSE
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                                                                                               13
30.131
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Mus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DONNELLY R.
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to: 332

genomic

analysis of

UZE G., LUTFALLA G.;
interferon/interleukin-10

V:0:

高門 原

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seq_name: sp_vertebrate:09YGC8
                                                                                                                       Q9YGC8, (TEMBLER, 10, C
01-MAY-1999 (TEMBLER, 10, I
01-MAY-1999 (TEMBLER, 10, I
01-MAY-1999 (TEMBLER, 10, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 CTARAGETTANAGCAGCACTA, CTTACGTCATGGRAAATT.
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                      663 .GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 .....ValPheHisGlyAlaThrPheGlnTyrLeuValHi 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 ATAAGAGCAGAAAAAGAAAAC...
SEQUENCE FROM N.A.
                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCTCGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 sTyrTrpGluLysSerGluThrGlnGlnGluGlnValGluGlyProPheL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TyrSerPhe
                                                                                                                                                                                                                                                                                                                                           sGlyLeuLeuSerAsnValSerCysHisGluThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oPheGlnHisTyrGluAsnValThrValGlyProProLysAsnIleSerV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 25:
                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....IleAspGlySerTrpH1sArgLe
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                                                                                                                                                Last sequence up
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                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....GTCGGGAATGTGACT 206
                                                                                                                                                                                                                                    341 AA.
                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                       Gallus.
                                                            Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1;
EMBL; AF082666; AAD13671.1;
                                              1301 ATGTGAGAAAACA 1313
                                                                                                                                                                                                                                                                                       1160 AAATGCTGAGAGAAAAATTATCGAG......AAAAAAACTGATGTTA 1200
                                                                                                                                                                                                                                                                                                                                                                                                         133 spPheThrGlyProAlaAlaAspArgGluHisAspLysTrpSerLeuLys 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 TGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                           150 GlnTyrTyrGlySerTrpTleTyrArgTleLeuTyrTrpLysLysGlySe 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGAT...... 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SerAspTrpAla:..ValValArgPheLysProMetAlaAspThrValIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 972 TCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             922 AAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 TGAAAATGTCAAAACTACCCAGTGT:::GTCTTTCCTCAAAACGTTTTCC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             825 AMANGGAATCCTGGAMACCATTTGTATAMATGGAMACAMATACCTGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        775 ATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LysGlnAsnPheAsnAsn.....ValTh 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 alargLysGlyAsnLeuSerTyrThrValGlnAlaLysSerIlePhePro 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 CysLeuLeuCysValSerGlyIleValProLysProArgAsnAlaAr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 .....GlyAlaTyrValLéuArgValArgThrGluTrpGluAspGluHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gIleSerSerValAsnPheArgSerValLeuLeuTrpAspProProGlyV 45
uCysGluglnThr 216: 2"
                                                                                                                          CACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGT 1300
                                                                                                                                                                                                       CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCA 1250
                                                                                                                                                                                                                                               rAsn....LysLysValIleHisileAspThrLysHisAsnSerGluI 181
                                                                                                                                                                                                                                                                                                                                                                   CAGGATTAT...CCACTGATTTATGAAATTATTTTTTGGGAAAACACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eGlyProProSerValAsnValLysSerGluSerGlyThrLeuH1sValA 133
                                                                                                                                                               leLeuSerGinLeuGluProTrpThrileTyrCysIleGinValGinGly 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                  .....VallleProGluTrpAsnLysThrGlyGluArgSerGlnGluLe 212
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1.469
58:371
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Gaps: 10
Percent Identity: 27.149
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seq_name: sp_vertebrate: Q9W6U9
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09W6U9;
01-NOV-1999 (TIEMBLIE1. 12, Created)
01-NOV-1999 (TIEMBLIE1. 12, Last sequence update)
01-NOV-1999 (TIEMBLIE1. 12, Last annotation update)
GLYCOPROTEIN 130 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEISSEN M... HELLER S., PENNICA D., ERNSBERGER U., ROHRER H.;
"The specification of sympathetic neurotransmitter phenotype depends or putokine receptor signaling.";
Development 125:4791-4801(1998).
EMBL; AJ011688; CAB42084.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 alAsnSerGlyIleLeuProThrValLeuLysLeuSerTrpGluAsnGln 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 TAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG...AACAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 TrpValGluAlaAlaAsnAlaLeuGlyLysAlaGluSerAspHisLeuVa, 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                    368 GTATGAGGTTGACTCATTTACACCATTTCGCAAAAGCTCAGATTGGTCCTC 417
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TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8).
                                                                                                                                                                                        330 TTGCGTATAAGAGCAGAAAAAGAAAAC.....ACTTCTTCATG 367
                                                                                                                                                                                                                                            284 roArgThrSerPheSerIleGlnGlyLeuArgProTyrThrGluTyrVal 300
                                                                                                                                                                                                                                                                                                                                                                                                  230 TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 IleSerThrValValMetGluLeuLysPheAsnIleArgTyrArgIleSe 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 AGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 lPheAspProIleGluIleValLysProProProProArgAsnLeuSerV 235
418 CAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT 467
                                                                                                                                                                                                                                                                                                    280 CCAPATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA 329
                                                                                                                                                                                                                                                                                                                                                268 rSerAspThrAsnTrpMetGluValProPro...GluAspThrAlaSerP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAT.....
                                                                                                                                        PheSerIleArgCysMetLysGluAspGlyValGlyPheTrpSerAspTr 317
                                                  pSerGlu..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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0.656.
46.374
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102495 MW; 9DC128C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..CTAAAATCTCCTCAA......AAAG
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Gaps: 24
Percent Identity: 20.220
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                                                  .....GluGlnIleGly....
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                                                       323
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330

97 KW

1192 CTGATGTTACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGAAA 1241   :::    :::        :::       :::       ::: 579 hrGluTyrThrLeuSerSerLeuThrSerAspThrLeuTyrThrValArg 595	GTGATTCATTCCATATC  GTGATTCATTCCATATC  TATATCGGTGCTCCAAAACAG	ATTTACCTTCTCCGCGT	796 TTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCAT 845 ::::::   457 yVallaGluTrpCysLeuMetSerAsnSerSerAspCys 470 846 TTGTATAAATGGAAACAATACCTGACTGTGAAAATGTCAAAACTACCCA 895 :::   :::   471 IleThrGluTrpGlnThrGluProGlyAsnIle	696 ACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCA 745 :::   :::     ::::	561 AGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAACTCTCA	468 CCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGC512
H	1 MetalaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgal 17  1 MetalaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgal 17  83 GGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 129  17 AGJUMetGlyThrAlaaspLeuGlyProSerSerValProThrProThrA 34  130 AAGTAGAGGTCGACATCATAAGATGACAACTTTATCCTGAGGTGGAACAGG 179  110 111 111 111 111 111 111 111 111 11		RP SEQUENCE FROM N.A.  RA DEMBIC Z.;  RA SUBMITTED (DEC-1994) to the EMBL/GenBank/DDBJ databases.  RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.  RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.  RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.  REMBL; U19241; AAC52064.1; JOINED.  REMBL; U19242; AAC52064.1; JOINED.  REMBL; U19245; AAC52064.1; JOINED.  REMBL; U19245; AAC52064.1; JOINED.  REMBL; U19246; AAC52064.1; JOINED.  SO SEQUENCE 484 AA; 53818 MW; EBC99D1F CRC32;	SEQUENCE FROM N.A. 97246734. VAN DER LEEDE B. J.M., TH W., ROMQUIN N., VIEGAS-1 Le for the ligand binding of the first 45:413-421(1997).	Homo sa Eukaryo Euther1 [1] SEQUENC MEDLINE AGUET M *MOlecu recepto Cell 55	1242 GCCAGAGCACACC 1256  I  :::    596 MetMetAlaTyrThr 600  seq_name: sp_human:Q14936  seq_documentation_block:

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seq_documentation_block:
ID 09YHV9 PRELIMINARY; PRT;
AC 09YHV9;
DT 01-MAY-1999 (TrEMBLrel: 10.) Created)
                                                                                                                                                  seq_name: sp_vertebrate:Q9YHV9
                                                                                                                                                                                                                                                                  1000 ATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGAT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            618 TATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
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                                                                                                                                                                                                    277 IleLeuProLysSerLeuIleSerValValArgSerAlaThrLeuGlu 292
                                                                                                                                                                                                                                                                                                                                                                                  950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               809 GCTCCACGCCTTTTAAAAAGGAATCCTGGAAACCATT.....TGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 erGluIleGlnTyrLysIleLeuThrGlnLysGluAspAspCysAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 CTATAGTCCAGTAC...ATTGTATAAAGACCACAGTTGAAAATGAACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                        258 uValPheIleCysPheTyrIleLysLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        900 GTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACA 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  765 AAAT.....GGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 CysTyrIleArgValTyrAsnVal.TyrValArgMetAsnGly.....S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy
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                                                                                                                                                                                                                                                                                                                                                                                  AGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTG 999
                                                                                                                                                                                                                                                                                                                       .....IleAsnProLeuLysGluLysSerIle 276
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                                                                   508 AA.
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           新・含くこっと: [1-2] 1842) [154] sLeüArgLysAsnGlyLysLeu.
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                                                                                                                                                                                                                                                                                         382 CATTTACACCATTTCGCAAAAGCTCAGATTGGTCCTCCAGAAGTACATTTA 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-1 x Q9YHV9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                            122 ... PheSerProLeuSerGluThrPheLeuGlyProProGluPheAsnLeu
                                                                                                                                                                                                                                                                                                                                                                             108 rPhevalGlyThrGluValPheAsnSerSerLeuLeuHis......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 .....ATCCTGAGGTGGAAC...AGGAGCGATGAGTCTGTCGGG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AATCTCCTCAAAAAGTA.....GAGGTCGACATCATAGATGACAACTTT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 508 AA;
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EMBL; AF082665; AAD13670.1;
HSSP; P13726; ITFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LIVER;
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477 .....AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACAT 519
                                                                        138 SerSerCysValHisCysIleAsnIleThrIleLysLeuProProThrH1 154
                                                                                                                                        432 GAAGCTGAAGATAAGGCAATAGTGATACACATCTCT...CCTGGAACA... 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 TCTTCACTCAAGCTGAATGTTTATGAAGAA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 GGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 yslleProArgGluProProAspAsnLeuGlnMetThrSerAsnAsnPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetGluThrLeuMetGlyGlyProLeuArgPheTyrGlnLeuValPheVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrAspAspPheGlnValValSerAspGluTyrSerAlaPheValGlnSe
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46.016
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Gaps: 29
Percent Identity: 21.116
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interferon/interleukin-10
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...GTATATTGTGTGAAAGCCAGA 1247

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388 tAspAlaGluGlu...........GluLysAspThrAspSerGluLeu....
                                                                                                                                                                                                                                                                                                                                                                342 eValArgArgAlaProGlnSerSerAspThrSerProValPheValGlnH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1160 AMATGCTGAGAGAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038 AACATTAGATCCCTTAGTGATTCATTCCATATCTATATC
                                                                                                                                                                                             1113 ... CAGGATTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTTC 1159
                                                                                                                                                                                                                                                                                                                                                                                                                 1077 ....... GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATC: ::::: 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          938 TCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAG 987
                                                                                                                                              376 ProAspAspGlyProGluValPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 yr.....TyrGlyIleThrIleAlaGlyAlaIleCysPheSerIle 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757 ATGTTCTTAAATGGGATTATACATATGCAAAC.....
                                                                                                                                                                                                                                                    359 isSerThrSerSerThrCysAspGlySerSerSerTrpValSerGlnAsn 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               988 AGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTT 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      888 ACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCT 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      707 TGAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657 AAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 ervalmetvalThrAlaSerLeuÁsnLysHisSerIleProSerAlaTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628 AAGTT.....AAAGCAGCACTACTTACGTCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           570 AATATTTATTCCAGACATAAA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520 ATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAA 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 hrLysMetPheSerTyrLeuProPheThrPheGluCysGluGluIleThr 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789 ....ATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 oPheSerIleVallleGluGluLeuTyrProAsnArgAsnTyrCysValS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spAspSerAspAspSerGluSerAspAlaMet......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ATTTATAAACTCTCACCAGAGACTACTTATTGTCTAA 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....SerAsnHisAspTyrThrArgArgAspIl 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....CysIleThrThrAsp.....
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                                                                                                                                        .GluAsnGluMe
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allgnment_block:
US-09-240-675-1 x p97798
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Ratio: 0.637
Percent Similarity: 49.157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_rodent:P97798
                                                                                                                __523 nProGlyGluMetGlnValThrIleGlnAsnLeuMetProAlaThrValT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 TIGTCCCCAGCCGCAGCTGGAAAAAATCTAAAATCTCCTCCAAAAAGTAGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1248 GCACAC 1253
                                                                                                                                                                                                                 511 GluGlyValAspArg.......GluArgValGluAsnThrSerGl 523
                                                                                                                                                                                                                                                                           228 ACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAG 277
                                                                                                                                                                                                                                                                                                                                                                       1.78. GGAGCGATGAGTCTGCGGAATGTGACTTTTTCATTCGATTATCAAAAA 227
                                                         310 ATGTTTATGAAGAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                      477. 1AlaSerLeuValSerThrArgPheIleLysLeuThrTrpArgThrProA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y09535; CAA70727.1; -. HSSP; P02751; lTTG. MGD; MGI:1097159; Neol.
                                                                                                                                                                                                                                                                                                                                  494 laSerAspProHisGlyAspAsnLeuThrTyrSerValPheTyrThrLys 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 GGTCGACATCATAGATGACAACTTTATC...CTGAGGTGGAAC......A 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1; 4.
PRINTS; PR00014; FNITYPEIII.
SEQUENCE 1493.AA; 163159 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 ..LeuSerProLeuSerLysValAsnCysThrTyrSerLeuArgSerArg 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 LeuAlaProAlaThrThrGlyProLeuProSerAlaProArgAspvalva 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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01-MAY-1997 (TremBLrel. 03,
01-NOV-1999 (TremBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EELING S.L., GAD J.M., COOPER H.M.;
MOUSE Neogenin, a DCC-like molecule, has four splice variants are expressed widely in the adult mouse and during embryogenesis.";
incogene 15:691-700(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                 .....ACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
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Gaps: 20
Percent Identity: 21.446
LysValMetAlaGlnAsaLysHisGly 551
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1206 CCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCA 1250
                                                                                                                                                                                                                                                                                                                                                                                                           1159 CAAATGCTGAGAGA...AAAATTATCGAGAAAAAAACTGATGTTACAGTT 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1109 GATCCAGGATTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGÄAACACGCCTGT 1108
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       828 GluAsnLeuAspProSerSerHisTyrValIleThrLeuLysAla 842
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PFAM; PF00047; 19; 3
PRINTS; PR00014; FNT)
SEQUENCE 1375 AA;
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FLYBASE; FBgn0011592;
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"ffazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is required for CNS and motor axon guidance."; Cell 87:197-204(1996).
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                       ProLeuGluValSerThrGlnProGluValAsnIleAlaGlyProProAr 563
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(TremBirel. 02, Last sequence update)
(TremBirel. 12, Last annotation update)
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                                                             ....ATAAGAGCAGAAAAAGAAAACACTTCTTCATGGT 369
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19	824	777 : ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTA
	866	849 uProValAspAlaProThrProLeuGluValProValGlyLeuArgAlaI
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	832	nMetAspTyrValValSerLeuArgAlaArgAsnVal
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	816	799 pGluAsnThrIleGluLeuLysGluThrGluArgTyrHisIleLeuLysA
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	799	LysileArgAsnTyrValLeuGlyTrpGlyArgGlyIleProAs
•	770	AGTGTCCAAAATCAGAACTATGTTCTTAAATGG
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	716	713 ACCT
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٠.	680	434 AGUTGARGATIARGGCAATAGTGATACACATUTCTCCUTGGAAAAAAG
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	596	snGlyGluIleLeuLysTyrArgValTyrT
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1032 SValGlnAlaArgThr 1037
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                                                                                                                                                                                                                                                                                                                                748 SerGluAsnAspSerGlyAlaAspLeuTyrHisAspSerThrAlaLeuGl 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0014; FNTYPEIII. SEQUENCE 1526 AA; 168787 MW; F17B1EC9 CRC32;
                                                                                                                                                                                      798 LysThrPheSerSerThrProSerGluProProAsnAsnValThrLeuGl
                                                                                                                                                                                                                                                                                   781 alProPheAsnArgAsnGlyMetGlyAspSerSerAlaGluIleArgVal 797
                                                                                                                                                                                                                                                                                                                                                                                 764 uAlaValLeuThrGluLeuArgProHisThrAspTyrValIleSerValV 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 ATGAG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 CGATTATCAAAAAACTGGGATGGATAAATTGGATAAAATTGTCTGGGTGTC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 rpValGluProLeuGlnAsnAlaGlyAspValValTyrTyrThrValTyr 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 GlyGlyLysProLeuAspSerGlyLeuGlnAlaArgLeuProSerGlnPr 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GGTGGAAAAATCTAAAATCT..........
831 luAspArgAsnGlyGlnIleThrGlyTyrLysIleArgTyrArgLys... 846
                                            481 ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTT 530
                                                                                                814 uValThrSerSerSerSerIleThrValH1sTrpGluProProAlaGluG
                                                                                                                                               434 A...GCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 gAsnPheGluGlyTyrAlaArgSerHisLysGluIleTyrValLysTrpG 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 lnPheArgValGluAlaAsnThrAsnPheGlySerGlyAlaSerSerAla 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648 TyrLysMetAsnAsnSerGluArgGluGlnLysMetValThrLysSerHi 664
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TCTTT	YrG] 3AAG	ATGTCAAAACTACCCAGTGTGTCTTTCC   ::   :::   :::   snThrThrAspLeuAsnCysMetIle:: snThrThrAspLeuAsnCysMetIle:::	CCTGGAA	AAAAGGAAT. :::::     AsnLysasnG	TAT	ovalas	1yAs	-	uGlu	uAsnT	Le Le		aAsn	spGluT	:	GGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGT::::::::::	aA1a	TTAAAGCAGCACTAC	rPheGluLeuSer	PheLy	ATCTGGAAAAA
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1 A	AAGCTTI	GTTT LeuA	TACC	rThr	GCTCCA  -::  -::	ovalgi	/sThr		uArga	ГутНі	LyArg	:	GlnH1			CAGTI	heThrG	ACGT	F-3	roAla	TGA
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                                                        228 ACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAG
                                                                                                                                                                                                                 449 alSerAspProGlnGlyAspAsnLeuThrTyrSerIlePheTyrThrLys 465
                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 LeuAlaProAlaThrThrGlyProLeuProThrAlaProArgAspvalva-432
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HSSP; P80362; 1WTL.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 19; 4.
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"Neogenin, an avian cell surface protein expressed during terminal neuronal differentiation, is closely related to the human tumor suppressor molecule deleted in colorectal cancer.";
J. Cell Biol. 127:2009-2020(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
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-NOV-1996 (TIEMBLrel. 01, Last sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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sValGlnAlaArgThr 1188
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738 SerIle...ValValSerTrpThrProProGluAsnGlnAsnIle...Va
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 ..... ClyThrHisSerGlyGlnfleThrGl 654
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                                                                                                                                                                                                                                              721 erArgValProGluValProSerSerLeuHisValArgProLeuValThr 737
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                                                                                                                                                                                                                                                                                                                                                    TCCTACTTCCTCCAGTC......TTTAACATTAGATCCCTTAGTGAT 105
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3550 C

.TrpileLys	45 lyGlnProValLysLeuAsnCysSerLeuGluGlyMetGluAspProGlu 61 45 ATCCTGAGGTGGAACAGCATGAGTCTGTCGGGAATGTGACTTTTC 211	LeuLeuGlyLeuTpalaAlaLeuArgaspGlyalav TGGAAAAATCTAAAATCTCCTCAAAAGTAGAGGTC TGGAAAAATCTAAAATCTCCTCAAAAGTAGAGGTC T		43:046 Percent Identity:	alignment_scores:  Quality: 123.00 Length: 453  Ratio: 0.631 Game: 25	PFA) PFA) PFA) SEQ	29049-29059(1996). 0041.1; - PROTEIN KINASE ATP;	SEQUENCE FROM N.A.  MEDLINE; 97067156: BISCARDI J.S., DENHEZ F., BUEHLER O'BRYAN J.P., DER C.'J.; FIORDALIS "Rek, a gene expressed in retina "Rek, a gene expressed in retina	OS Gallus gallus (Chicken). OS Gallus gallus (Chicken). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. RN [1]	DT 01-FEB-1997 (TrEMBLrel. 02, Created) DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) DE AXL-RELATED RECEPTOR TYROSINE KINASE.	seq_name: sp_vertebrate:Q98949 seq_documentation_block: ID Q98949 PREVIMINARY; PRT; 873 AA.	1206 CCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCA 1250                 :::     ::: ::    782 GluasnleuaspproSerSerHisTyrValileThrLeuLysala 796	1159 CAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTT 1205 :::   :::    :::    ::: 765 roHisAlaGinThrileLysValAspTyrLysGlnArgTyrTyrThrile 781	1109 GATCCAGGATTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTT 1158  ::::::     :::     ::::::::::::::::::
1007 AATACAAGCTTTCCTACTTCCTCAGTCTTTAACATTAGAF6CCTTAGTG 10	931 TI TACCTTCTCCGCGTACAAGCATCT 9  1.	ਵ <b>਼ਾ</b> ਮੁ'	227 erAsnAlaSerValValTrpValProGlyPheAspGlyArgAla 2 834 CCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAA 8	TVALSET CANACATTORAGITORAGITORAGITANANAGANT CANACATGACCTTTCANGTTCAGTGGCTCCACGCCTTTTANANAGGANT CHALLES CONTINUE	215 PROPROLEGASINATTA GENERAL PROPROLEGASINATTA 2 734 AGTEAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATG 7	634 AAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATACGTCAGTACAT 6   -	584 ACATAAAATTTÄTAAACTÖTCACCAGAGACTACTTÄTTGTCTAAAAGTTA 6    ::::::	160 alriptipMetGlyAspSerArgValGlyLeuProAsplleSerProSer 1 540ACTCTTCAGGTGTAGAAGAAGGATTGAAAATATTTATTCCAG 5 [         ::::::::::::::::::::::::::::	143 OPheHisMetAlaCysAlaAlayalGlyProProGluProValThrIleV 1 529 TTATCTGGAAA 5	4.29 IIANAMOTISANGATANGGCAATAGTGATAAAA 4.29 IIANAMOTISANGAAA 4.29 IIANAMOTISANGAAA 4.29 IIANAMOTISANGATANGGCAATAGTGATAAAA 4.29 IIANAMOTISANGGCTTTGGATGGTTTAAGCTTTACATATAGCTTAC 5.479 AGATAGGTTAAGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTAC 5.479 AGATAGGTTAAGGGCTTTGGATGGTTTAAGCTTACATATAGCTTAC 5.479 AGATAGGTTAAGGGTTTAAGGTTTAAGGTTAAGAGTTAAGGTTAAGAGTTAAGGTTAAGAGTTAAGGTTAAGAGAGAGTTAAGAGAGAGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GCAAAGCTCAGATTGGTCCTCCAGAAGTACAT	356 CACTICATICATGGTATGAGGTTGACTCATTTACACCATTTC 3  11	306 CIGAAIGITTAIGAAGAAATTAAAITGCGTATAAGAGCAGAAAAAGAAAA 94 ServalGluar 9	256 CIGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAG 3

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alignment_scores
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485 gValGluAğnThrSerHisPröGlyGluMetGlnValThrIleGlnAsnL 503
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                                           242 TTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACT 291
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                                                                                                  470 AsnLeuThrTyrSerValPheTyrThrLysGluGlylleAlaArgGluAr 486
                                                                                                                                         198 AATGTGACTITITCATICGATTATCAAAAAACTGGGATG......GATAA 241
                                                                                                                                                                                                                                                                                                                      436
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                                                                                                                                                                                                                                                                                                                                                                                                                    425 LeuIleIleLeuGluHisAlaPro..........AlaThrThrGl
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                   rgPheIleLysLeuThrTrpArgThrProAlaSerAspProHisGlyAsp 469
                                                                                                                                                                                                                                         ACTITATE...CTGAGGTGGAAC::...AGGAGCGATGAGTCTGTCGGG 197
                                                                                                                                                                                                                                                                                                      yProLeuProSerAlaProArgAspyalyalAlaSerLeuValSerThrA
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EB-1997 (TrEMBLrel. 02, Last sequence update)
OV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: Q92859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17263.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOOK A.T., BIGNER S.H., FEARON E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159958 MW; 0AB7247E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HING THE SEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 20.665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 to: 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAAACCACTGACTGTA... 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1461 AA
                                                                                                                                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
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                                                                                                                                                                                                                                                                                                                                                                                                                         436
Service 36 Control of the Service 762 mass Glands nile... Valvalar gGlyTyrAlaileGlyTyrGlyTig
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CAGGATTATCCACTGATTATGAAATTA 1140	1091 GTCTGGAAACACGCCTGTGATCCAGGATTATCC
CCATATCTATATCGGTGCTCC	CATATC
CTTCCTCCAGTC	0 ATACTGAAATACAAGCTTTCCTACTTCCTC 1
CTTTTTGGTCTGAAGAGATAAAGTTTG, 999	CTTTTTGG
~ O	AGGAATTTACCTTC     YThrGluTyrAsnF
reteanactacccaetetetetetete. 908 :::    :::    serGinLeuile	AAACI
AATCCIGGAAACCATTIGTATAAATGGA 858	CCTGG ValTh
CAAACATGACCTTCAAGTTCAGTG 808	AACAT
.CAGAACTAIGTTCTTAAATGGGAT 773	730 TAGAAGTCAGTGTCCAAAATCAGAACTATC
SAAAATGAACTACCTCCACCAGAAAATA 729 	680 ACATTGTATAAAGACCACAGTTGAAAATGAACT
CATGGAAAATTGGTGTCTATAGTCCAGT,679 ::        y8HisGlyProGlyValSerThrProAs 623	630 GITAAAGCAGCACTACITACGTCATGGAAAATT
CTCACCAGAGACTACTTATTGTCTAAAA 629	580 CCAGACATAAAATTTATAAAACTCTCACCAGAG :::             ::: 592 isSerTyrThrileAsnGlyLeuLysLysTyrT
STAGAAGAAAGGATTGAAAATATTTATT 579    ::::::::::::::::::::::::::::::::::	AAG     :
AIGGITTAAGCTITACATATAGCTTACT 529 ::    snGlyGluIleGlnAsnTyrLysLeuTy 575	GGTTTAAG      GlyGluIl
TCCTGGAACAAAAGATI :    ::: aSerProThrSerIle	ρ· i-j
CCTCCAGAAGTACATTTAGAAGCTGAAG 441          ::    	CCAGAAG         ProGluy
CATGGTATGAGGTTGACTCATTTACACC 391 :::    :::   1yGluSerSerAlapr 527	GGTATG
FINITGAGAAATTAAATTGCCTATAAGA 341 ELL ARGYALMET 514	he AT

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alignment_scores: 122.50 Quality: 122.50 Ratio: 0.581 Percent Similarity: 50.119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: 000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-240-675-1 x 000340
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292 TTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791 GlnArgTyrThrIleGluAsnLeuAspProSerSerHisTyrValIl 807
                                               486 gValGluAsnThrSerHisProGlyGluMetGlnValThrIleGlnAsnL 503
                                                                                                   242 TTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACT 291
                                                                                                                                                                                      198 AATGTGACTTTTCATTCGATTATCAAAAAACTGGGGATG.....GATAA 241
                                                                                                                                                                                                                                                453 rgPheileLysLeuThrTrpArgThrProAlaSerAspProHisGlyAsp 469
                                                                                                                                                                                                                                                                                          157 ACTITATC...CTGAGGTGGAAC.....AGGAGCGATGAGTCTGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 LeuileileLeuGluHisAlaPro.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      807 eThrLeuLysala 811
                                                                                                                                                                                                                                                                                                                                              436 yProLeuProSerAlaProArgAspValValAlaSerLeuValSerThrA 453
                                                                                                                                                                                                                                                                                                                                                                                        107 AAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 CTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IELMETTER J., CHENG X.N., MISKEVICH F., LANE R.P., YAMAKAWA K., ORENBERG J.R., DREYER W.J.;
Molecular characterization of human neogenin, a DCC-related protein, mod the mapping of its gene (NEO1) to chromosomal position 15q22.3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE-BRAIN;
EDLINE; 97312699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUENCE FROM N.A.
                                                                                                                                             AsnLeuThrTyrSerValPheTyrThrLysGluGlyIleAlaArgGluAr 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAGCCAGAGCA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0014; FNTYPEIII.
1461 AA; 160015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 421
Gaps: 20
Percent Identity: 20.665
                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaThrThrG1 436
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       湖南
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777	762 uAsnGlnAsnIleValValArgGlyTyrAlaIleGlyTy <del>r</del> GlyIle.	
1140		
1090	ATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACA :::	
746		
999 730		
958 713		
908	859 AACAAATACCTGACTGTGAAAAATGTCAAAACTACCCAGTGTGTCTTTCCT	•
858 690	TAȚAAATGGA ::: ValSerGlyT	
808 673	GIG :::	
773 656	730 TAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGAT	,
729 640	680 ACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATA :::::::::::::::::::::::::::::::	
679 623	630 GTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGT	
629 608	580 CCAGACATAAAAİTTATAAACICTCACCAGAGACTACTTATTGTCTAAAA	
579 592	CAGGTGTAGAAGA ::    :: hraspLysGluGl	
529 575	492 TGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT	
491 558	442 ATAAGGCAATAGTGATACACATCTCCCTGGAACAAAAGATAGTGTTATG :::         ::: ::	
441 542	392 ATTICGCAAAGCICAGAATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAG	
391 527	342 GCAGAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCC	
514	503 eumetProAlaThrValTyrIlePheArgValMet	

1141 TITITIGGGAAAACACITCAAAIGCIGAGAGA...AAAAITAICGAGAAA 1187

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SO DE RETERENTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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US-09-240-675-1 x Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg_1/1 to: Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block:
Q91562 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1238
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                                                                                                                                                                                                                                                                                                                                                                                   447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 TCTCCTCAAAAGTAGAGGTCGACATCATAGATGACAACTTTATC...CT 166
  506 snGlu
                                            349 AAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGC
                                                                                                                                       314 T....
                                                                                                                                                                                          481 GlnProlle...
                                                                                                                                                                                                                                                                                                                                                                                                                          167 GAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 AlaProArgAspValValProValLeuValSerSerArgPheValArgLe 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                    264 CAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGT 313
                                                                                                                                                                                                                                                                                464 alTyrPheSerLysGlnGlyValGlnArgGluArgAlaValAsnThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAM; PF00041; fn3; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U10986; AAA70168.1;
HSSP; P56276; 1TLK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDLINE; 95113183.

"IERCEALL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Express<sub>1</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-NOV-1996 (TIEMBLIEL.
L-NOV-1996 (TIEMBLIEL.
L-NOV-1999 (TIEMBLIEL.
MOR SUPPRESSOR.
                                                                                                                                                                                                                                                                                                                                  TCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGT 263
                                                                                                                                                                                                                                                                                                                                                                                uSerTrpArgProProValGluSerLysGlyAsnIleGlnThrTyrThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eThrLeuLysAla 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ression of a homologue of the deleted in colorectal cancer (DCC) in the nervous system of developing Xenopus embryos.";
Biol. 166:654-665(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_vertebrate:Q91562
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0.596
47.017
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                                                                                                                                         TATGAAGAAATTAAATTGCGTATAAGAGCAGAAA 348
                                                                                                                                                                                   TrpGlyProGlyGluSerSerGlnGluValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01, Created)
01, Last sequence update)
12, Last annotation update)
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Gaps:
Percent Identity:
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22.196
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Xenopodinae;
                                            398
                                                                                                                                                                                                                                                                                   480
                                                                                                                                                                                                                                                                                                                                                                                464
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       7.655....GlySerProTyrAlaGluThrValArgValAspSerLysGlnArg
                                                                                                                                                                                                                                                                                                                                                        1005
                                                               1147 GGGAAAACACTTCAAATGCTGAGAGA...AAAATTATCGAGAAAAAACT 1193
                                                                                                                                                 1097 AAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTTT 1146
                                                                                                                                                                                                                                                                                                    719 spleuAspGluSerGlnValProAspGlnProSerSerLeuHisValArg
                                                                                                                                                                                                                                                                                                                                                                                                  702 nGlyThrGlyProSerSerAspTrpTyrThrAlaGluThrProGluAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                              965 TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACT.....
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                                                                                                                                                                                                              736 ProLeuThrThrSerIle...IleMetSerTrpThrProProLeuAsnPr 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 LeuGluLysGlySerGlnTyrSerPheGlnValAlaAlaMetThrValAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              921 ... CAAAAAGGAATT... TACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             669 lyGluLeuGluThrLeuGluProAsnAsnLeuTrpTyrLeuPheThrGly 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  766 AATGGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCAC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 aMetProGlnAsnValSerLeuGluValAlaAsn......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 ValValThrGlnProGluLeuGlnValProGlyProValGluAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 TARATGGARACARATACCTGACTGTGARARTGTCARARCTACC..... 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 TCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 ValSerSerGluGluHisThrValValThrLeuSerAspValProSerAl 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 GTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 luTyrSerIleArgValLeuAla.....TyrAsnArgTyrGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                616 CTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 eGluValAspGlyIleValTyrArgLeuGluGlyLeuArgLysPheThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 TGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 GlyTyrArgLeuPheCysAlaGluThrPheSerGlyArgGluGlnAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        519 ... TATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGAT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 ..
                                                                                                            oAsnIle...ValValArgGlyTyrIleIleGlyTyrGlyVal.....
                                                                                                                                                                                                                                                             TCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGG
                                                                                                                                                                                                                                                                                                                                                   .....GAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....CAGTGTGTCTTTCCTCAAAACGTTTTC........
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780 TyrTyrSerIleGluAsnLeuGluProSerSerHisTyrValIleSerLe 796

1244 CAGAGCA 1250 :::||| 796 uLysAla 798

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